Transcriptional network analysis in frontal cortex in Lewy body diseases with focus on dementia with Lewy bodies

Gabriel Santpere PhD[1,2*], Paula Garcia-Esparcia PhD[3*], Pol Andres-Benito MsC[3], Belen Lorente-Galdos PhD[1,2], Arcadi Navarro PhD[2,4,5,6], Isidro Ferrer MD, PhD[3,7,8,9]

* These authors contributed equally

[1] Department of Neurobiology, Yale School of Medicine, New Haven, Connecticut, USA

[2] Department of Experimental and Health Sciences, IBE, Institute of Evolutionary Biology, Universitat Pompeu Fabra-CSIC, Barcelona, Spain

[3] Department of Pathology and Experimental Therapeutics, University of Barcelona, L'Hospitalet de Llobregat, Spain

[4] Centre for Genomic Regulation (CRG), Barcelona, Spain

[5] National Institute for Bioinformatics (INB), Barcelona, Spain

[6] Institució Catalana de Recerca i Estudis Avançats (ICREA), Barcelona, Spain

[7] Institute of Neuropathology, Service of Pathologic Anatomy, IDIBELL-Hospital Universitari de Bellvitge, Hospitalet de Llobregat, Spain

[8] Institute of Neurosciences, University of Barcelona, Hospitalet de Llobregat, Spain

[9] CIBERNED, Network Centre for Biomedical Research of Neurodegenerative Diseases, Institute Carlos III, Spain

CA: Prof. Isidro Ferrer Department of Pathology and Experimental Therapeutics, University of Barcelona, campus Bellvitge, c Feixa LLarga sn, 08097 Hospitalet de Llobregat, Spain Phone: +34 93 4035808; email: 8082ifa@gmail.com

Compliance with ethical standards No relevant data; no conflicts of interest

Number of words: 5988

Number of figures: 4

Number of tables: 2

Supplementary material: 7 supplementary tables

This article has been accepted for publication and undergone full peer review but has not been through the copyediting, typesetting, pagination and proofreading process which may lead to differences between this version and the Version of Record. Please cite this article as an 'Accepted Article', doi: 10.1111/bpa.12511

Abstract

The present study investigates global transcriptional changes in frontal cortex area 8 in incidental Lewy Body disease (iLBD), Parkinson disease (PD) and Dementia with Lewy bodies (DLB). We identified different co-expressed gene sets associated with disease stages, and gene ontology categories enriched in gene modules and differentially expressed genes including modules or gene clusters correlated to iLBD comprising upregulated dynein genes and taste receptors, and down-regulated innate inflammation. Focusing on DLB, we found modules with genes significantly enriched in functions related to RNA and DNA production, mitochondria and energy metabolism, purine metabolism, chaperone and protein folding system, and synapses and neurotransmission (particularly the GABAergic system). The expression of more than fifty selected genes was assessed with RT-qPCR. Our findings provide, for the first time, evidence of molecular cortical alterations in iLBD and involvement of several key metabolic pathways and gene hubs in DLB which may underlie cognitive impairment and dementia.

Key words: Lewy body diseases, dementia with Lewy bodies, cerebral cortex, transcriptome, mitochondria, synapses, neurotransmission, GABA, purine metabolism, chaperones, dynein, axonema, taste receptors

Introduction

Lewy body diseases (LBDs), which include Parkinson's disease (PD) and dementia with Lewy Bodies (DLB), are neurodegenerative disorders, characterized by the presence of intracytoplasmic neuronal inclusions named Lewy bodies (LB) and abnormal neurites containing α-synuclein species and aggregates (32, 41, 46, 49, 64). Non-motor symptoms such as sleep disorders, loss of olfaction and autonomic alterations may precede the appearance of motor symptoms; cognitive impairment and dementia can occur at advanced stages of PD, and dementia is compulsory in DLB. Braak stages of α-synuclein pathology distribution are useful to delineate a framework to interlink LBDs into a spectrum. Stages 1-3 can be associated with pre-motor symptoms although in most cases the presence of LBs and neurites in selected regions of the medulla oblongata, pons and midbrain is an incidental finding at autopsy. The term incidental PD or LBD (iPD or iLBD) refers to those early stages of LBD pathology with no apparent clinical symptoms, corresponding to the early stages of LBD spectrum (23). PD is usually manifested at stages 4 and 5 once the involvement of the substantia nigra reaches determinate thresholds of neuronal loss and dopaminergic denervation of the striatum is manifested. Cognitive impairment can be detected at stages 5 and 6 in PD, whereas DLB cases are categorized as Braak stages 5 and 6 of LB pathology (11, 87). However, no exact correlation exists between Braak stages and clinical symptoms linked to cognitive impairment and dementia (14, 24, 28, 47, 48, 65, 77), this fact suggesting that factors other than LBs and neurites play a cardinal role in the pathogenesis of LBDs. Concomitant pathologies, particularly those linked to Alzheimer’s disease, have also been suggested to explain variations in the degree of cognitive impairment in DLB (8, 17, 47, 50, 70, 71).

Decreased dopaminergic, noradrenergic serotoninergic and cholinergic innervation of the cerebral cortex are contributory factors to the appearance of cognitive impairment and dementia in PD. They are due to the loss of vulnerable neurons in the substantia nigra, locus coeruleus, raphe nuclei and nuclei of the basal forebrain including the basal nucleus of Meynert, respectively (13, 43, 45, 53, 54, 62, 89). However, recent studies demonstrate the primary impairment of several metabolic pathways in the cerebral cortex in PD and other LBDs, such as synaptic transmission, mitochondria and energy metabolism, purine metabolism, protein synthesis, lipid composition of membranes, and inflammation, among others (19, 20, 26, 28, 30, 33, 34, 37, 61, 63, 68, 74, 79, 94).

Studies of transcriptomic profiling in LBDs have been mainly focused on the typically affected sub-cortical regions such as substantia nigra, locus coeruleus and striatum in PD (8, 18, 40). Cortical regions have received much less attention with studies limiting their outcome to lists of differentially expressed genes (DEGs) (59). Still, this approach has allowed the discovery of the brain expression of olfactory and taste receptors and their de-regulation in the cerebral cortex and substantia nigra in PD (38, 42).

Here, we set out to investigate global transcriptomic changes occurring in the frontal cortex of cases of iLBD, PD and DLB relative to middle-aged individuals with no neurological symptoms and with no alterations at the post-mortem examination. We focused particularly on identifying gene co-expression modules showing correlation with the spectrum of LB disorders. By applying weighted gene co-expression network analysis (WGCNA) (57) to microarray data, we determined the transcriptome structure in the frontal cortex and identified co-expression modules correlated to iLBD, PD and DLB. Validation of hubs and selected altered pathways was carried out with RT-qPCR.

Material and methods Brain samples

Brain tissue was obtained from the Institute of Neuropathology Brain Bank (HUB-ICOIDIBELL Biobank) and the Hospital Clinic-IDIBAPS Biobank following the guidelines of Spanish legislation on this matter and of the local ethics committee. Processing of brain tissue has been detailed elsewhere (31, 80). The post-mortem interval between death and tissue processing was between 3h and 15h. One hemisphere was cut in 1- cm-thick coronal sections, and selected areas of the encephalon were rapidly dissected, frozen on metal plates over dry ice, placed in individual air-tight plastic bags, numbered with water-resistant ink and stored at -80.C until use for biochemical studies. The other hemisphere was fixed by immersion in 4% buffered formalin for 3 weeks for morphologic studies. Neuropathological diagnosis was categorized following current staging classifications for LBD (1, 10, 78). For Alzheimer’s disease (AD)-related pathology, neurofibrillary tangles (NFTs) (9) and phases of AD-related β-amyloid plaques (91) were assigned. Only cases with “typical” staging of LBD pathology were selected for study.

Two series of cases were used. The first one served for microarray studies. RNA samples from frontal cortex (area 8) of middle aged (MA) (n = 8, 4 men, 4 women; age: 67.5 ± 12.8 years), iLBD (n=4, 1 men, 3 women; age: 71.2 ± 4.5 years), PD (n = 8, 4 men, 4 women, age: 67.8 ± 8.8 years) and DLB (n=8, 5 men, 3 women; age: 72.3 ± 8.6) cases were analyzed using the Affymetrix microarray platform and the Genechip Human Gene 1.1 ST Array (Affymetrix, Santa Clara, CA, USA). The second series of cases was used for RT-qPCR validation of altered expression of selected genes. Cases used for gene validation were iLDB (n=5, 4 men, 1 woman; age: 66.8 ± 8.9 years) at stages 3 and 4, and PD cases (n=9, 3 men, 6 women; age: 77.1 ± 4.7 years) at stages 5 and 6, DLB cases (n=9, 8 men, 1 woman; age 76.44 ± 5.77 years). PD cases had suffered from parkinsonism and had received treatment during the duration of the disease but did not have dementia. MA cases had not suffered from neurological disease and the neuropathological examination did not reveal abnormalities (n=15, 6 men, 9 women, age 64.4 ± 15.5 years). In addition, four cases with rapid clinical course DLB (rpDLB; two years of less of disease duration) (2 men and 2 women, age 73.7 ± 2.2 years) were chosen for a few selective studies (35, 36).

Cases with associated pathologies such as vascular diseases (excepting mild atherosclerosis and arteriolosclerosis), TDP-43 proteinopathy, infection of the nervous system, brain neoplasms, systemic and central immune diseases, metabolic syndrome and hypoxia were excluded from the present study. Regarding AD-related pathology, rare NFTs and β-amyloid deposits were found in iLBD (Braak stages 0-II; Thal phases

0-I); Braak stages I-III and Thal phases 0-3 were observed in PD; Braak stages 0-V and Thal phases 0-5 occurred in DLB. MA cases had not suffered from neurologic, psychiatric or metabolic diseases (including metabolic syndrome), and did not have abnormalities in the neuropathological examination excepting NFT pathology stages I-II and phases 0-2 of β-amyloid plaques.

RNA extraction

Purification of RNA was carried out with RNeasy Lipid Tissue Mini Kit (Qiagen, Hilden, Germany) following the protocol provided by the manufacturer. During purification, samples were treated with RNase-free DNase Set (Qiagen) to avoid later amplification of genomic DNA. The concentration of each sample was obtained from A260 measurements with Nanodrop 1000. RNA integrity was tested using the Agilent 2100 BioAnalyzer (Agilent Technologies, Santa Clara, CA, USA). Values of RNA quality (RIN values) were from 7 to 8.8 in the first series and from 6.2 to 8.2 in the second series.

Microarray analysis

Affymetrix microarray platform and the Genechip Human Gene 1.1 ST Array was used to analyze gene expression patterns on a whole-genome scale on a single array with probes covering several exons on the target genes. Starting material was 200ηg of total RNA from each sample. Sense ssDNA was generated from total RNA with the Ambion WT Expression Kit from Ambion (Carlsbad, CA, USA), according to the manufacturer’s instructions. Sense ssDNA was fragmented, labelled and hybridized to the arrays with the GeneChip WT Terminal Labeling and Hybridization Kit from Affymetrix. Chips were processed on an Affymetrix GeneTitan platform.

Pre-processing of raw data and statistical analyses were performed using Bioconductor packages in R programming environment. We read CEL files from Affymetrix arrays, corrected the background, and summarized and normalized the data with the robust microarray method implemented in the Bioconductor Limma package (81). Then, fold change and SEs were assessed by fitting a linear model (using the lmFit function in Limma package) for each gene. Genes with empirical Bayes t test p values at a level of 0.01 were selected. Multiple testing correction was performed by adjusting P-values for false discovery rate (FDR) using the Benjamini and Hochberg method (BH).

Gene enrichment score

The average expression values of different transcripts of the same gene were used for gene enrichment scores and weighted gene co-expression network analysis. Only genes in the upper 25% percentile of standard deviation of expression among samples were assessed. For probes mapping to multiple genes we fused all gene ids into one and that was considered a ‘gene’ in the network analysis but not for functional annotation, GO enrichment and PPI analysis, for which all individual ids were used.

An enrichment score per gene (5), which is a measure of specificity of a gene for a particular group, disease state in our study, was calculated relative to the rest of the groups tested. Briefly, the method is based on computing linear model coefficients contrasting all groups pair-wise. These coefficients represent a measure of difference between two groups in which more distant categories present higher coefficient values usually associated with lower p-values. The enrichment score of a gene in a group is the sum of its significant coefficients against all other groups.

The enrichment score for each of the 5,114 genes under study was calculated after obtaining the linear models for microarray data with the LIMMA package (81) considering a linear coefficient statistically significant at uncorrected p-value lower than 0.01.

Weighted gene co-expression network analysis

WGCNA was done in R using the WGCNA library (57). We first constructed a gene coexpression network based on pair-wise correlation of gene expression using all samples at the same time or independently for each disease condition. Not all network topologies fitted with the scale-free topology model (i.e., the iLBD network). Therefore, all subsequent analysis based on the co-expression network constructed with all samples used a soft-power threshold of 5. We identified modules of genes based on their topological overlap dissimilarity with their connection strengths in the weighted network (44, 66). Using the dynamic tree-pruning algorithm, 23 initial modules were obtained; genes not assigned to any module were labelled in grey. After merging all modules with highly correlated eigengenes (Pearson correlation >/= 0.8), 13 final modules were obtained. Module eigengenes were correlated to LBD diagnostic. The P-values were obtained from a general multivariate lineal model including additional control variables (i.e. age, sex, RIN, PMI and batch).

Gene enrichment analysis Gene ontology enrichment analysis was performed using GOstats (27). Differentially expressed genes with uncorrected p-values <0.01 for each contrast were used for GO analysis. All genes belonging to a particular gene co-expression module were also used for independent GO analyses. P-values for categories were adjusted considering FDR using BH with the p.adjust function in R.

Protein-protein interaction network

Assumed protein-protein interaction was obtained with BioGrid, latest release. Subnetworks of genes were obtained using the function-induced subgraph from the R library rTRM (74). Only nodes with evidence of physical interaction in humans were considered. Networks were analyzed and visualized using Cytoscape (86).

Real-time PCR

Real-time quantitative PCR (RT-qPCR) assays were conducted in duplicate on 1,000ηg of cDNA samples obtained from the retrotranscription reaction, diluted 1:20 in 384-well optical plates (Kisker Biotech, Steinfurt, GE) utilizing the ABI Prism 7900 HT Sequence Detection System (Applied Biosystems). Parallel amplification reactions were carried out using 20x TaqMan Gene Expression Assays and 2x TaqMan Universal PCR Master Mix (Applied Biosystems). TaqMan probes used in the study are shown in Supplementary Table 1. The reactions were performed using the following parameters: 50.C for 2 min, 95.C for 10 min, 40 cycles at 95.C for 15 sec and at 60.C for 1 min. TaqMan PCR data were captured using the Sequence Detection Software (SDS version 2.2, Applied Biosystems). Subsequently, threshold cycle (CT) data for each sample were analyzed with the double delta CT (ΔΔCT) method. First, delta CT (ΔCT) values were calculated as the normalized CT values for each target gene in relation to the endogenous controls β-glucuronidase (GUS-β) and X-prolyl aminopeptidase P1 (XPNPEP1). These housekeeping genes were selected because they show no modifications in several neurodegenerative diseases in human postmortem brain tissue (4, 25). A similar pattern was observed using GUS-β and XPNPEP1 for normalization (data not shown). The mean of GUS-β and XPNPEP1 was used for correction and representation. Finally, ΔΔCT values were obtained with the ΔCT of each sample minus the mean ΔCT of the population of control samples (calibrator samples). The fold-change was determined using the equation 2-ΔΔCT (38).

Statistical analysis for RT-qPCR

The normality of distribution of the mean fold-change values obtained with RT-qPCR for every region and stage between controls and PD cases was analyzed with the Kolmogorov-Smirnov test. The non-parametric Mann-Whitney test was performed to compare each group when the samples did not follow a normal distribution and the unpaired student’s T-test was used for normal variables. Statistical analysis was performed with GraphPad Prism version 5.01 (La Jolla, CA, USA) and Statgraphics Statistical Analysis and Data Visualization Software version 5.1 (Warrenton, VA, USA). Differences between groups were considered statistically significant at P-values: *p < 0.05, **p < 0.01 and ***p < 0.001. Additionally, BH-FDR adjusted p-values were obtained using the p.adjust function in R.

Results

Differential gene expression and gene enrichment score in frontal cortex area 8 in iLBD, PD and DLB

We contrasted gene expression values of all possible pair-wise comparisons among all diagnostic groups. We selected differentially expressed genes or DEGs (see methods). We found most DEGs occurred between DLB and the rest of groups; in particular, most were genes down-regulated in DLB compared to controls, followed by genes upregulated in DLB. Considering nominal p-values lower than 0.01, PD and iLBD showed fewer DEGs than DLB. Considering multiple-testing adjusted p-values < 0.05, only DLB cases produced DEG genes comparable to controls, and no gene survived that threshold in iLBD and PD (Supplementary Table 2).

We performed gene ontology (GO) enrichment analysis focused on biological process categories for each group of DEGs independently in up- and down-regulated genes (Supplementary Table 3).

To summarize all pair-wise group comparison in one statistic, we calculated a gene enrichment score for each of the 5,114 genes analyzed. The advantage of this approach is the possibility of highlighting genes that are differentially expressed in one group relative to all other groups. The score of a given gene summarizes differences in expression levels between comparisons among all four groups of samples. Positive or negative scores are associated with an increase or a reduction in expression, respectively, of each gene in a given group relative to the rest of the groups. We obtained 1,914 genes with an enrichment score other than 0 in at least one of the groups. As revealed by clustering analysis, we found that DLB presented the highest number of genes with higher enrichment scores (Figure 1a). In agreement with the proportion of DEGs described above, gene scores in DLB were mostly negative (Figure 1a). The fifty top up-regulated and top down-regulated genes in DLB are listed in Supplementary Table 4.

The main up-regulated genes in frontal cortex in iLBD were associated with axonemal dynein complex assembly and taste receptors, whereas the main down-regulated genes were linked to inflammation (Table 1a).

The main up-regulated genes in frontal cortex in DLB compared with controls were categorized into cellular development and DNA/RNA metabolism genes. The main down-regulated genes in frontal cortex in DLB compared with controls were grouped into synapsis and neurotransmission, chaperone and protein folding, mitochondria and energy metabolism, purine metabolism and inflammation (Table 1b).

Weighted gene co-expression network analysis

Weighted gene co-expression network was constructed using the expression values of 5,114 genes with variable expression among the 28 samples. Thirteen uncorrelated (r<0.8 gene modules were identified and labelled by colours and numbers (M1 to M13). The genes not assigned to any particular co-expression module were assigned to M0 or ‘grey’ (Figure 1b).

We obtained the most representative pattern of gene expression across all samples for each one of these modules by calculating the eigengene (i.e., the first principal component). The eigengene of each module was then correlated with the LBD spectrum (iLBD, PD and DLB) obtaining an eigengene significance for each module (Figure 2a). Three modules, M4-lightcyan (157 genes), M6-tan (215 genes) and M10-darkred (23 genes) were negatively correlated with iLBD. M3-green (226 genes), M11-royalblue (23 genes) were positively, and M10-darkred negatively, correlated to PD were negatively correlated with iLBD. M3-green (226 genes) and M11-royalblue (23 genes) were positively, and M10-darkred negatively, correlated to PD. Three other modules, M3-green, M5-brown and M9-salmon, correlated significantly with DLB. M5-brown correlated negatively with DLB and contained 766 genes. M3-green and M9-salmon correlated positively with DLB and contained 226 and 51 genes, respectively (Figure 2b). None of our identified disease-correlated modules were also correlated with age, indicating that our disease associated modules are not significantly confounded by transcriptomic changes produced by normal ageing. Of note, one module, M7-midnightblue, was negatively correlated with age.

Module characterization

Four strategies were used: 1) Identification of top highly connected genes (or hubs) in each module, 2) Assessment of overlaps with available published brain modules to correlate present LBD-associated modules to brain-related biological categories, 3) Identification of enriched GO among genes in each module, and 4) Subdivision of each module into sub-networks based on available knowledge concerning physical protein-protein interactions (PPI) networks of human proteins.

Top hub genes

MSN, UGT2B11, LAPTM5 gene was the top hub genes in the iLBD-associated modules M4-lightcyan, M10-darkred and M6-tan, respectively. MSN encodes for Moesin, a molecule that links cytoskeleton to membrane and which is a suggested phosphorylation target of LRRK2. UGT2B11 encodes a UDP-glucuronosyltransferase and LAPTM5 is a lysosomal gene recently identified as a hub node in the protein-interaction network obtained from DEGs in locus ceruleus in PD patients versus healthy donors (18). Hub genes in M3-green and M11-royalblue, PD-associated modules, are genes with unknown function. ATP6V1B2 and ATP6V1A, and STIP1 were top hub genes for M5-brown and M9- salmon, respectively, linked to DLB modules. ATP6V1A encodes a component of vacuolar ATPase which mediates the acidification of intracellular organelles including endosomes, lysosomes, the trans-Golgi network, and synaptic vesicles, thus enabling a plethora of functions such as zymogen activation, endocytosis, synaptic transmission and protein transport (12). STIP1 (HOP) is implicated in assisting the function of chaperone protein interaction with HSP70 and HSP90 (72) (Supplementary Table 5).

Overlap of modules with reported brain-related categories: specific cell populations and particular diseases

Module M6-tan and M4-lightcyan were highly enriched in markers of microglia (65). M5- brown and M9-salmon DLB-associated modules were found enriched in neuronal and microglial markers (14, 57) (Figure 3, Supplementary Table 6). Other modules identified in our study, but not correlated with LBD, showed enrichment in particular cell types. For instance, M2-blue module was enriched in oligodendrocyte markers whereas M1-cyan and M7-midnightblue were enriched in neuronal and glial cell markers. These observations support the biological consistency of our network and the robustness of the method to build similar transcriptomic modules using different sources of data.

M6-tan modules presented enrichment in genes that was also de-regulated at early stages of AD (75). Moreover, module M5-brown showed overlap with de-regulated gene sets and modules reported in AD (6, 60). These confluences suggest commonalities involving multiple processes in these neurodegenerative diseases. In fact, DLB is largely associated with AD-related pathology, and DLB cases in the present series had associated AD pathology.

Identification of enriched GO among genes in each module

We also attempted to relate genes in modules to particular GO. Consistent with the microglial nature of this module, genes in M6-tan were highly enriched in GO categories related to immune system and inflammation. Similarly, M4-lightcyan was also enriched in categories related to inflammatory defence response. Module M5-brown showed highly significant enrichment in GO categories related to synaptic transmission and energy metabolism, among others. Genes in M9-salmon module presented a highly significant enrichment in GO categories related to protein folding and heat-shock chaperone activity. Interestingly, the age associated M7-midnightblue module was enriched in GO categories such as hormone response, oxidative stress and learning, among others. Supplementary Table 7 shows the full list of categories in modules 3, 5, 6, 9 and 11. Only few genes composed M11-royalblueand M10-darkred for proper GO analysis, but those modules contained taste receptors (TAS2R10, TAS2R4, TAS2R50) and nine olfactory receptors, respectively.

Putative sub-networks of protein-protein interactions

We intersected genes from each co-expression module with protein-protein interaction (PPI) databases to identify putative sub-networks with biological relevance within modules. Genes in M6-tan, M4-lightcyan, M5-brown and M9-salmon each produced notable PPI subnetworks composed of 44, 51, 302 and 21 genes, respectively (representing 25.7%, 35.4%, 47.2% and 45.7% of the genes in the module listed in the PPI database). Regarding M6-tan module PPI sub-network, spleen tyrosine kinase (encoded by SYK) appeared with 16 interacting partners as the nucleating gene with highest degree (Figure 4a). M4-lightcyan included a sub-network with CDK2, MSN and TP53 as top degree nodes (Figure 4b). Heat-shock related proteins encoded by genes STIP1, HSPA5, AHSA1 and HSPA1A were the highest connected nodes in the M9-salmon PPI sub-network (Figure 4c). M5-brown module contained a large PPI sub-network with several nodes including proteins encoded by YWHAB, TP1A, GSK3B, PSMA3 and SNCA, among others (Figure 4d).

These results allow for better characterization of selected LBD-associated modules. M5-brown globally down-regulated in DLB and enriched in neuronal markers and in genes mostly related to synaptic transmission and energy metabolism presented ATP6V1B2 and YWHAB as top hub genes in the transcriptomic and PPI networks, respectively. Other highly connected molecules were GSK3B, PSMA3, ATP6V0D1, TPI1, ATP6V1A and SNCA. Finally, an M9-salmon module, globally up-regulated in DLB, was characterized by significant enrichment in genes involved in heat-shock protein folding and microglial markers, and was nuclearized around the hub gene STIP1 in both transcriptomic and PPI networks. Other highly interacting proteins were encoded by DNAJA1, DNAJB1, DNAJB4, HSPA5, HSAPA6, AHSA1 and HSPA1A.

RT-qPCR validation

LAPTM5, a top gene in M6, was found not to be de-regulated in iLBD, PD and DLB. ATP6V1A, one of the top genes in M5, was down-regulated in DLB (1.03 ± 0.25 vs 0.57 ± 0.52, p = 0.007). The expression of STIP1, one top gene in M9, was not significantly altered in DLB but only in a subset of rpDLB (see later) and in PD (1.03 ± 0.28 vs 1.75 0.70, p = 0.006); however, mRNA expression of DNAJA1 and DNAJB1, other top genes in the same module, was significantly increased in DLB (see later). SYK, the principal PPI in M6 was not de-regulated in iLBD, PD and DLB (MA: 1.06 ± 0.51, iLBD: 0.81 ± 0.58, PD: 1.02 ± 0.38, DLB: 1.47 ± 0.93).

TPI1, a PPI member of module 5, was up-regulated in PD (1.02 ± 0.20 vs 1.29 ± 0.14, p = 0.004). No significant modifications in the expression mRNA levels were observed for selected PPI members of M5 and M9 modules in DLB. However, several members were de-regulated in a sub-population of DLB cases characterized by their rapid course and classified as rpDLB. Regarding M5, up-regulated genes in rpDLB were GSK3B (1.03 ± 0.22 vs 1.62 ± 0.88, p =0.046), whereas PSMA3 (1.01 ± 0.15 vs 0.57 ± 0.05, p =0.000) and YWHAB (1.01 ± 0.15 vs 0.69 ± 0.22, p = 0.007) were downregulated. Genes representative of PPI in M9 were up-regulated in rpDLB: HSPA1A (1.01 ± 0.40 vs 3.10 ± 2.00, p=0.007), HSPA5 (1.06 ± 0.38 vs 2.14 ± 0.83, p=0.003) and STIP1 (1.03 ± 0.28 vs 2.07 ± 1.10, p=0.009).

Abnormal regulation of the dynein cluster was assessed by RT-qPCR in LBDs with particular attention on iLBD. TASRs were assessed in iLBD, PD and DLB. Three biological functions, RNA/DNA metabolism, chaperone and protein folding, and synaptic neurotransmission, were selected for validation in DLB. We extracted those pathways and clusters from each of those categories that appeared in the corresponding module and disease in which the category appeared as significantly enriched.

Regarding dyneins, DNAAF1, DNAH11, DNAH2, DNAH7 and DNAI1, but not DNAH5 and DNAH9, were significantly up-regulated in iLBD when compared with MA. Interestingly, up-regulation also occurred in PD and DLB. Taste receptor TAS2R5 and TAS2R13 were up- and down-regulated, respectively, in iLBD; TAS2R10 up-regulated in PD, and TAS2R4, TAS2R5, TAS2R14, TAS2R10 and TAS2R13 significantly up-regulated in DLB (Table 2a).

Moving on to iLBD, expression of AIF1 (which encodes IBA-1) was down-regulated, as predicted, in frontal cortex (control: 1.07 ± 0.41, iLBD: 0.57 ± 0.20, p = 0.018). Focusing on DLB, PNPT1, PAPOLA, RELA and DOT1L mRNAs, all of them involved in RNA/DNA metabolism, but not KAT2A, were significantly up-regulated in DLB (Table 2b). Importantly, PNPT1 and RELA were up-regulated in iLBD, and KAT2A was added in PD (Table 2b).

Chaperone members DNAJA1, DNAJA4, DNAJB1, HSPA4, HSPA6 and HSPD1, but not DNAJB4, HSPA1A, HSPA5 and HSPE1, were significantly up-regulated in frontal cortex area 8 in DLB when compared with MA (Table 2b). No modification in the expression of these genes was found in iLBD, but DNAJA1, HSPA4 and HSPA5 mRNA expression was significantly increased in PD (Table 2).

Finally, neurotransmission-related components GABBR2, GABRA1, GAD1, and synaptic proteins neuropilin and tolloid-like 1 (NETO1), as well as synaptophysin (SYP) mRNAs, were found to be significantly down-regulated in DLB when compared with MA. The expression of GRIN2A and GRIN2B, and synaptic proteins RAB3A, RPH3A, SNAP25, STXBP1, SYT1, SYT13 and SYT16, was not altered in DLB (Table 2b).

Discussion

This study presents the first transcriptome analysis of the frontal cortex integrating the whole spectrum of LBDs. In addition to performing a traditional gene-based differential expression analysis we considered a system biology approach based on co-expression networks. In particular, we applied WGNCA which allows the identification of modules of genes that are co-expressed across samples. These modules have to be interpreted with the understanding that such co-expression reflects a common biological function (e.g., from biochemical pathways to cell type defining signatures). We have identified some modules that correlate with LBDs. A proportion of genes included in those modules are also differentially expressed in a traditional gene-based comparative approach using the same microarray data and using independent case series for RTqPCR quantification and validation. The present study has also identified several hubs and PPI which raise the alert about putative biomarkers and targets for therapeutic intervention.

Lack of co-morbidities in the present series implies the selection of a limited number of cases which minimizes the risk of bias. PD and DLB cases have concomitant AD-related pathology which was variable from one case to another. Thal phases were used to evaluate β-amyloid plaques; however no distinction was made between diffuse and neuritic plaques.

Discussion is centred on selected genes, among those identified by differential expression analysis and weighted correlation networks, whose mRNA expression was assessed with RT-qPCR. The transcriptome is relatively conserved in iLBD and PD as no genes surpass the threshold of significance when p-values are adjusted for multiple testing. This is in contrast with DLB where hundreds of genes show multiple testing-corrected significant expression differences when compared with MA individuals.

Dyneins are one de-regulated cluster in LBDs. Five of seven assessed members are up-regulated in iLBD and PD, and three of seven in DLB. Because of their ATP hydrolysis-mediated involvement in cytoplasmic transport (82), early alteration of the cargo transport along neurites may be suggested in the frontal cortex within the LBD spectrum.

Expression of taste and olfactory receptors and down-stream obliged functional signalling pathways in the CNS and their de-regulation in neurodegenerative diseases is intriguing. It is possible that these receptors in brain are not involved in the perception of odours and taste but rather correspond to new central chemoreceptors looking for putative ligands or interacting complementary receptors (29). TASRs are significantly up-regulated in frontal cortex in PD and DLB (36, 38), and our findings further indicate that de-regulation of TASRs in frontal cortex occurs in iLBD as well.

Previous studies have shown altered protein synthesis machinery in the frontal cortex in PD and DLB from the nucleolus to the ribosome (34, 36). Nuclear alterations include increased nucleolar stress and altered synthesis of ribosomal RNAs, in addition to altered production of mRNAs. Our findings show altered mRNA expression of different molecules involved in RNA and DNA metabolism such as KAT2A which is up-regulated in PD, and PNPT1, PAPOLA, RELA, and DOT1Ls which are up-regulated in DLB. PNPT1 and RELA are also up-regulated in iLBD. Therefore, genes which encode proteins involved in the acetylation and methylation of histones, RNA processing and the modulation of NF-κB-mediated gene transcription are abnormally regulated in DLB and, to a lesser degree, in other disorders within the LBD spectrum. A primary effect of α-synuclein can be postulated, as α-synuclein is abnormally localized in the nucleus in neurons, and probably also in glial cells, in the frontal cortex in PD (34).

Another de-regulated cluster in LBD is related to innate inflammatory responses. This has been the subject of two detailed studies in PD and DLB (36, 37). An interesting aspect was the down-regulation of cytokines and several mediators of the inflammatory response in the substantia nigra at early stages of PD (37) and the relatively low inflammatory response in the frontal cortex in DLB (36), which is in line with previous observations pointing out the relatively low inflammatory response and enhanced dystrophic microglia in DLB (2, 88, 90). This is further supported in the present study by down-regulation of AIF1, which encodes the microglial marker IBA-1 in the frontal cortex in iLBD, thus suggesting early microglial alteration in LBDs.

Another DLB-associated module is related to heat-shock/chaperone proteins and is globally up-regulated in DLB. Three out of ten assessed genes are up-regulated in the frontal cortex in PD and six out of ten in DLB. These include DNAJA1, DNAJ4 and DNAJB1, the products of which act as heat shock protein 70 co-chaperones, and chaperones HSPA4, HSPA6 and HSPD1.

Moreover, STIP1, a co-partner in the HSP70/HSP90 activity in protein folding, is the top hub gene in this module and PPI together with HSPA1A and HSPA5. DNAJA1 and DNAJB1 are also among the top hub genes in this module. Importantly, the expression of this gene is increased in PD and DLB but significantly up-regulated only in PD. Refolding and clearance of α-synuclein aggregates requires chaperones and the proteasome system (55). Our findings are consistent with the presence of abnormally aggregated α-synuclein in the cortex in DLB and also with previous observations of increased folding proteins and unfolded protein response in DLB (3, 16).

We found a large gene co-expression module down-regulated in DLB that is enriched in neuronal markers and in genes mainly involved in synaptic transmission. Synapses are altered in the cortex in PD and DLB (19, 20, 74, 84, 85). α-synuclein is abundant in the pre-synaptic terminals, where it plays a role in synaptic function. Abnormal folding and oligomerization and formation of certain types of aggregates may directly produce synaptic damage, and may do so indirectly by exerting toxicity on mitochondria, lysosomes and cytoskeleton (56, 74, 84). Notably, a top degree gene of the PPI subnetwork from this module is α-synuclein. In spite of being a PPI hub, SNCA is not a DEG between DLB and CTL as assessed by Limma, which highlights the importance of the present higher-complexity level study in revealing genes otherwise veiled in conventional differential expression methods.

Gene down-regulation related to neurotransmission in the frontal cortex in DLB particularly involves GAD1, the product of which catalyzes the synthesis of γ-aminobutyric acid from L-glutamic acid, and GABA receptors GABBR2 and GABRA1, showing that the GABAergic system in frontal cortex is vulnerable to DLB. Other downregulated genes are NETO1, which encodes a protein involved in synaptic N-methyl-Daspartic acid receptor complexes, and SYP, which encodes synaptophysin, a major synaptic protein. In line with the present findings, loss of post-synaptic GABAreceptor markers has been reported in the occipital cortex in DLB (52). Synaptophysin expression was previously reported as decreased in the occipital cortex in DLB as well (67). The identification of de-regulated M5 top hub gene, ATP6V1A, the product of which mediates the acidification of several intracellular organelles including synaptic vesicles, thereby facilitating synaptic transmission (12), further points to altered synaptic function.

Other altered pathways identified in the M5-brown module, namely energy metabolism and mitochondrial function, and purine metabolism, have been the subject of previous analysis. Mitochondria and energy metabolism is altered in the frontal cortex in PD and DLB (35, 36, 51, 68, 69, 76, 92). Moreover, decreased enzymatic activity of complexes I, II, II and IV has been demonstrated in a subset of PD cases with dementia (36, 69) and in cases with DLB (35, 68). Abnormal α-synuclein is localized in mitochondria in the frontal cortex in PD (36) and in the nucleus (34); thus, a possible link between altered nuclear and mitochondrial DNA/RNA processing and aberrant α-synuclein may be considered. The present study also shows two additional PPIs in module 5. CYCS encodes a small heme protein localized in the inner membrane of the mitochondria which transports electrons from cytochrome b to the cytochrome oxidase complex (21). Secondly, TPI1 encodes a protein which participates in glycolysis and glucogenesis (93).

Regarding purine metabolism, our previous RT-qPCR studies revealed abnormal expression of several enzymes involved in purine metabolism in PD and DLB (33, 36). No attempt was made to validate other important altered pathways such as those inked to the ubiquitin proteasome system (UPS) in LBDs revealed by microarrays, and interpretation of significantly altered regulation of certain top hub genes in M5 such as GSK3B and YWHAB, and M6 as LAPTM5 remains speculative.

Concluding comments

The study of human cases is irreplaceable in the effort to gain understanding of the neurodegenerative diseases that are exclusive to human beings. It can be criticized the limited number of available cases suitable for molecular studies in the present series. This limitation may account for certain discrepancies between the observations obtained with arrays and the subsequent validations with RT-qPCR, and also by the observation of isolated deregulated genes which are apparently disconnected from highly represented de-regulated clusters. In spite of these constraints, the present study, using selected samples with no co-morbidity and adequate RNA preservation, has documented an extraordinary amount of information. Validation of the present findings should be expected in other independent series.

We used a 'network medicine' approach to the study of LBDs aiming at unveiling changes in the transcriptome in frontal cortex area 8 which may affect particular metabolic pathways and biological functions. This approach is being increasingly used to discover relevant pathogenic effectors in neurodegenerative diseases (83). Here we show early alteration in the regulation of the axonema and particularly of dyneins, and of taste receptors in iLBD, maintained and augmented along with the progression of the LBD spectrum. Interestingly, innate inflammation is down-regulated in iLBD as manifested by decreased AIF1 expression. It is worth mentioning that the expression of several cytokines and mediators of the inflammatory response is also reduced in iLBD (unpublished observations); the small number of cases assessed in this series precludes further evaluations, but our findings provide insights that will allow deepening to into the study of reduced innate inflammatory regulation at early stages of LBDs. We have also identified and validated de-regulation of several pathways in the frontal cortex in DLB; this includes up-regulation of RNA/DNA processing and chaperones, and down-regulation of neurotransmission thereby revealing the vulnerability of the GABAergic system. Altered mitochondria and energy metabolism, protein synthesis, and altered purine metabolism regulation were the subject of previous studies. Our approach has also identified robust de-regulated modules represented by several genes, hub genes and PPI sub-networks within these modules. These observations reveal potential candidates for further analysis as they may involve key pathogenic molecular events taking place in the frontal cortex in LBDs.

Acknowledgements

This study was funded by the Ministerio de Econom.a y Competitividad, Instituto de Salud Carlos III – Fondos FEDER, a Way to Build Europe FIS (grant PI14/00757 to IF and grants BFU-2012-38236 and BFU-2015-68649-P to AN), by the Spanish National Institute of Bioinformatics of the Instituto de Salud (PT13/0001/0026) and by FEDER (Fondo Europeo de Desarrollo Regional)/FSE (Fondo Social Europeo), and coordinated Intraciber 2014: Rapid Dementias. We wish to thank Gerard Muntané. for technical assistance and valuable discussion and T. Yohannan for editorial help.

Author's contribution GS performed WGCNA, PG-E carried out RT-qPCR, PA-B the analysis of arrays, BL-G performed the gene enrichment score analysis, AN refined the design, IF designed the study, selected the cases, supervised the work and wrote the manuscript which was circulated among all the authors to add comments and suggestions. All the authors agreed with the contents of the manuscript.

References

1. Alafuzoff I, Ince PG, Arzberger T, Al-Sarraj S, Bell J, Bodi I, Bogdanovic N, Bugiani O, Ferrer I, Gelpi E, Gentleman S, Giaccone G, Ironside JW, Kavantzas N, King A, Korkolopoulou P, Kovács GG, Meyronet D, Monoranu C, Parchi P, Parkkinen L, Patsouris E, Roggendorf W, Rozemuller A, Stadelmann-Nessler C, Streichenberger N, Thal DR, Kretzschmar H. (2009) Staging/typing of Lewy body related alphasynuclein pathology: a study of the BrainNet Europe Consortium. Acta Neuropathol 117: 635-52.

2. Bachstetter AD, Van Eldik LJ, Schmitt FA, Neltner JH, Ighodaro ET, Webster SJ, Patel E, Abner EL, Kryscio RJ, Nelson PT (2015) Disease-related microglia heterogeneity in the hippocampus of Alzheimer's disease, dementia with Lewy bodies, and hippocampal sclerosis of aging. Acta Neuropathol Commun 3: 32.

3. Baek JH, Whitfield D, Howlett D, Francis P, Bereczki E, Ballard C, Hortobágyi T, Attems J, Aarsland D (2016) Unfolded protein response is activated in Lewy body dementias. Neuropathol Appl Neurobiol 42: 352–65.

4. Barrachina M, Castaño E, Ferrer I (2006) TaqMan PCR assay in the control of RNA normalization in human post-mortem brain tissue. Neurochem Int 49: 276-84.

5. Benita Y, Cao Z, Giallourakis C, Li C, Gardet A, Xavier RJ (2010) Gene enrichment profiles reveal T-cell development, differentiation, and lineage-specific transcription factors including ZBTB25 as a novel NF-AT repressor. Blood 115: 5376-5384.

6. Blalock EM, Geddes JW, Chen KC, Porter NM, Markesbery WR, Landfield PW (2004) Incipient Alzheimer’s disease: microarray correlation analyses reveal major transcriptional and tumor suppressor responses. Proc Natl Acad Sci USA 101: 2173-21738.

7. Botta-Orfila T, Sànchez-Pla A, Fernández M, Carmona F, Ezquerra M, Tolosa E (2012) Brain transcriptomic profiling in idiopathic and LRRK2-associated Parkinson’sdisease. Brain Res 1466: 152-157.

8. Boyle PA, Yu L, Wilson RS, Gamble K, Buchman AS, Bennett DA (2012) Poor decision making is a consequence of cognitive decline among older persons without Alzheimer's disease or mild cognitive impairment. PLoS One 7: e43647.

9. Braak H, Braak E (1991) Neuropathological staging of Alzheimer-related changes. Acta Neuropathol 82: 239-259.

10. Braak H, Del Tredici K, Rüb U, de Vos RA, Jansen Steur EN, Braak E (2003) Staging of brain pathology related to sporadic Parkinson's disease. Neurobiol Aging 24: 197-211.

11. Braak H, Rüb U, Del Tredici K (2006) Cognitive decline correlates with neuropathological stage in Parkinson's disease. J Neurol Sci 248: 255-258.

12. Breton S, Brown D (2013) Regulation of luminal acidification by the V-ATPase. Physiology 28: 318-329.

13. Buddhala C, Loftin SK, Kuley BM, Cairns NJ, Campbell MC, Perlmutter JS, Kotzbauer PT (2015) Dopaminergic, serotonergic, and noradrenergic deficits in Parkinson disease. Ann Clin Transl Neurol 2: 949-959.

14. Burke RE, Dauer WT, Vonsattel JP (2008) A critical evaluation of the Braak staging scheme for Parkinson's disease. Ann Neurol 64: 485-491.

15. Cahoy JD Emery B, Kaushal A, Foo LC, Zamanian JL, Christopherson KS, Xing Y, Lubischer JL, Krieg PA, Krupenko SA, Thompson WJ, Barres BA (2008) A transcriptome database for astrocytes, neurons, and oligodendrocytes: a new resource for understanding brain development and function. J Neurosci 28: 264-278.

16. Cantuti-Castelvetri I, Klucken J, Ingelsson M, Ramasamy K, McLean PJ, Frosch MP, Hyman BT, Standaert DG (2005) Alpha-synuclein and chaperones in dementia with Lewy bodies. J Neuropathol Exp Neurol 64: 1058-1066.

17. Colom-Cadena M, Gelpi E, Charif S, Belbin O, Blesa R, Martí MJ, Clarimón J, Lleó A (2013) Confluence of α-synuclein, tau, and β-amyloid pathologies in dementia with Lewy bodies. J Neuropathol Exp Neurol 72: 1203-1212.

18. Cui S Sun H, Gu X, Lv E, Zhang Y, Dong P, Fu C, Zhu C (2015) Gene expression profiling analysis of locus coeruleus in idiopathic Parkinson's disease by bioinformatics. Neurol Sci 36: 97-102.

19. Dalfó E, Albasanz JL, Martin M, Ferrer I (2004) Abnormal metabotropic glutamate receptor expression and signaling in the cerebral cortex in diffuse Lewy body disease is associated with irregular alpha-synuclein/phospholipase C (PLCbeta1) interactions. Brain Pathol 14: 388-398.

20. Dalfó E, Barrachina M, Rosa JL, Ambrosio S, Ferrer I (2004) Abnormal alphasynuclein interactions with rab3a and rabphilin in diffuse Lewy body disease. Neurobiol Dis 16: 92-97.

21. Delgado JY, Owens GC (2012) The cytochrome c gene proximal enhancer drives activity-dependent reporter gene expression in hippocampal neurons. Front Mol Neurosci 5: 31.

22. Diez D, Hutchins AP, Miranda-Saavedra D (2014) Systematic identification of transcriptional regulatory modules from protein-protein interaction networks. Nucleic Acids Res 42: e6.

23. Dickson DW, Fujishiro H, DelleDonne A, Menke J, Ahmed Z, Klos KJ, Josephs KA, Frigerio R, Burnett M, Parisi JE, Ahlskog JE (2008) Evidence that incidental Lewy body disease is pre-symptomatic Parkinson's disease. Acta Neuropathol 115: 437-444.

24. Dickson DW, Uchikado H, Fujishiro H, Tsuboi Y (2010) Evidence in favor of Braak staging of Parkinson's disease. Mov Disord 25 Suppl 1:S78-82.

25. Durrenberger PF, Fernando FS, Magliozzi R, Kashefi SN, Bonnert TP, Ferrer I, Seilhean D, Nait-Oumesmar B, Schmitt A, Gebicke-Haerter PJ, Falkai P, Grünblatt E, Palkovits M, Parchi P, Capellari S, Arzberger T, Kretzschmar H, Roncaroli F, Dexter DT, Reynolds R (2012) Selection of novel reference genes for use in the human central nervous system: a BrainNet Europe Study. Acta Neuropathol 124: 893-903.

26. Fabelo N, Martín V, Santpere G, Marín R, Torrent L, Ferrer I, Diaz M (2011) Severe alterations in lipid composition of frontal cortex lipid rafts from Parkinson's disease and incidental Parkinson's disease. Mol Med 17: 1107-1118.

27. Falcon S, Gentleman R (2007) Using GOstats to test gene lists for GO term association. Bioinformatics 23: 257-258.

28. Ferrer I (2009) Early involvement of the cerebral cortex in Parkinson's disease: convergence of multiple metabolic defects. Prog Neurobiol 88: 89-103.

29. Ferrer I, Garcia-Esparcia P, Carmona M, Carro E, Aronica E, Kovacs G, Grison A, Gustincich S (2016). Olfactory receptors in non-chemosensory organs: the nervous system in health and disease. Front Aging Neurosci 8: 163.

30. Ferrer I, López-Gonzalez I, Carmona M, Dalfó E, Pujol A, Martínez A (2012) Neurochemistry and the non-motor aspects of PD. Neurobiol Dis 46: 508-526.

31. Ferrer I, Martinez A, Boluda S, Parchi P, Barrachina M (2008) Brain banks: benefits, limitations and cautions concerning the use of post-mortem brain tissue for molecular studies. Cell Tissue Bank 9: 181-194.

32. Fujishiro H, Ferman TJ, Boeve BF, Smith GE, Graff-Radford NR, Uitti RJ, Wszolek ZK, Knopman DS, Petersen RC, Parisi JE, Dickson DW (2008) Validation of the neuropathologic criteria of the third consortium for dementia with Lewy bodies for prospectively diagnosed cases. J Neuropathol Exp Neurol 67: 649-56.

33. Garcia-Esparcia P, Hernández-Ortega K, Ansoleaga B, Carmona M, Ferrer I (2015) Purine metabolism gene deregulation in Parkinson's disease. Neuropathol Appl Neurobiol 41: 926-940.

34. Garcia-Esparcia P, Hernández-Ortega K, Koneti A, Gil L, Delgado-Morales R, Castaño E, Carmona M, Ferrer I (2015) Altered machinery of protein synthesis is region- and stage-dependent and is associated with α-synuclein oligomers in Parkinson's disease. Acta Neuropathol Commun 3: 76.

35. Garcia-Esparcia P, Koneti A, Rodríguez-Oroz MC, Lago B, del Rio JA, Ferrer I (2017) Mitochondrial activity in the frontal cortex area 8 and angular gyrus in Parkinson's disease and Parkinson's disease with dementia. Brain Pathol, in press.

36. Garcia-Esparcia P, López Gonzalez I, Grau-Rivera O, García-Garrido MF, Konetti A, Llorens F, Zafar S, Carmona M, del Rio JA, Zerr I, Gelpi E, Ferrer I (2017) Dementia with Lewy bodies: age-related molecular pathology in the frontal cortex in typical and rapidly progressive forms. Frontiers Neurol, accepted for publication

37. Garcia-Esparcia P, Llorens F, Carmona M, Ferrer I (2014) Complex deregulation and expression of cytokines and mediators of the immune response in Parkinson's disease brain is region dependent. Brain Pathol 24: 584-98.

38. Garcia-Esparcia P, Schlüter A, Carmona M, Moreno J, Ansoleaga B, Torrejón-Escribano B, Gustincich S, Pujol A, Ferrer I (2013) Functional genomics reveals dysregulation of cortical olfactory receptors in Parkinson disease: novel putative chemoreceptors in the human brain. J Neuropathol Exp Neurol 72: 524-539.

39. Gatt AP, Duncan OF, Attems J, Francis PT, Ballard CG, Bateman JM (2016) Dementia in Parkinson's disease is associated with enhanced mitochondrial complex I deficiency. Mov Disord 31: 352-359.

40. Glaab E, Schneider R (2015) Comparative pathway and network analysis of brain transcriptome changes during adult aging and in Parkinson's disease. Neurobiol Dis 74: 1-13.

41. Goedert M (2001) Alpha-synuclein and neurodegenerative diseases. Nat RevNeurosci 2: 492-501.

42. Grison A, Zucchelli S, Urzì A, Zamparo I, Lazarevic D, Pascarella G, Roncaglia P, Giorgetti A, Garcia-Esparcia P, Vlachouli C, Simone R, Persichetti F, Forrest AR, Hayashizaki Y, Carloni P, Ferrer I, Lodovichi C, Plessy C; FANTOM Consortium, Carninci P1, Gustincich S (2014) Mesencephalic dopaminergic neurons express a repertoire of olfactory receptors and respond to odorant-like molecules. BMC Genomics 15: 729.

43. Grothe MJ, Schuster C, Bauer F, Heinsen H, Prudlo J, Teipel SJ (2014) Atrophy of the cholinergic basal forebrain in dementia with Lewy bodies and Alzheimer's disease dementia. J Neurol 261: 1939-1948.

44. Hawrylycz MJ, Lein ES, Guillozet-Bongaarts AL, Shen EH, Ng L, Miller JA, van de Lagemaat LN, Smith KA, Ebbert A, Riley ZL, Abajian C, Beckmann CF, Bernard A, Bertagnolli D, Boe AF, Cartagena PM, Chakravarty MM, Chapin M, Chong J, Dalley RA, Daly BD, Dang C, Datta S, Dee N, Dolbeare TA, Faber V, Feng D, Fowler DR, Goldy J, Gregor BW, Haradon Z, Haynor DR, Hohmann JG, Horvath S, Howard RE,

Jeromin A, Jochim JM, Kinnunen M, Lau C, Lazarz ET, Lee C, Lemon TA, Li L, Li Y, Morris JA, Overly CC, Parker PD, Parry SE, Reding M, Royall JJ, Schulkin J, Sequeira PA, Slaughterbeck CR, Smith SC, Sodt AJ, Sunkin SM, Swanson BE, Vawter MP, Williams D, Wohnoutka P, Zielke HR, Geschwind DH, Hof PR, Smith SM, Koch C, Grant SG, Jones AR (2012) An anatomically comprehensive atlas of the adult human brain transcriptome. Nature 489: 391-399.

45. Huang SH, Chang CC, Lui CC, Chen NC, Lee CC, Wang PW, Jiang CF (2015) Cortical metabolic and nigrostriatal abnormalities associated with clinical stage-specific dementia with Lewy bodies. Clin Nucl Med 40: 26-31.

46. Ince PG (2011) Dementia with Lewy bodies and Parkinson's disease with de6entia. In: Neurodegeneration, the molecular pathology of dementia and movement disorders, Dickson DW, Weller RO (eds), pp. 224-237, Wiley-Blackwell, Oxford

47. Jellinger KA (2007) Morphological substrates of parkinsonism with and without dementia: a retrospective clinico-pathological study. J Neural Transm 72: 91-104.

48. Jellinger KA (2009) Significance of brain lesions in Parkinson disease dementia and Lewy body dementia. Front Neurol Neurosci 24: 114-125.

49. Jellinger KA (2011) Parkinson's disease. In: Neurodegeneration: the molecular pathology of dementia and movement disorders, Dickson DW, Weller RO (eds), pp. 194-233, Wiley-Blackwell, Oxford.

50. Jellinger KA, Attems J (2008) Prevalence and impact of vascular and Alzheimer athologies in Lewy body disease. Acta Neuropathol 115: 427-436.

51. Keeney PM, Xie J, Capaldi RA, Bennett JP (2006) Parkinson's disease brain mitochondrial complex I has oxidatively damaged subunits and is functionally impaired and misassembled. J Neurosci 26: 5256-5264.

52. Khundakar AA, Hanson PS, Erskine D, Lax NZ, Roscamp J, Karyka E, Tsefou E, Singh P, Cockell SJ, Gribben A, Ramsay L, Blain PG, Mosimann UP, Lett DJ, Elstner M, Turnbull DM, Xiang CC, Brownstein MJ, O'Brien JT, Taylor JP, Attems J, Thomas AJ, McKeith IG, Morris CM (2016) Analysis of primary visual cortex in dementia with

Lewy bodies indicates GABAergic involvement associated with recurrent complex visual hallucinations. Acta Neuropathol Commun 4: 66.

53. Kim HJ, Lee JE, Shin SJ, Sohn YH, Lee PH (2011) Analysis of the substantia innominata volume in patients with Parkinson's disease with dementia, dementia with Lewy bodies, and Alzheimer's disease. J Mov Disord 4: 68-72.

54. Klein JC, Eggers C, Kalbe E, Weisenbach S, Hohmann C, Vollmar S, Baudrexel S, Diederich NJ, Heiss WD, Hilker R (2010) Neurotransmitter changes in dementia with Lewy bodies and Parkinson disease in vivo. Neurology 74: 885-92.

55. Klucken J, Shin Y, Masliah E, Hyman BT, McLean PJ (2004) Hsp70 Reduces α-synuclein aggregation and toxicity. J Biol Chem 279: 25497-25502.

56. Kramer ML, Schulz-Schaeffer WJ (2007) Presynaptic alpha-synuclein aggregates, not Lewy bodies, cause neurodegeneration in dementia with Lewy bodies. J Neurosci 27: 1405-1410.

57. Langfelder P, Horvath S (2008) WGCNA: an R package for weighted correlation network analysis. BMC Bioinformatics 9: 559.

58. Lein ES, Hawrylycz MJ, Ao N, Ayres M, Bensinger A, Bernard A, Boe AF, Boguski MS, Brockway KS, Byrnes EJ, Chen L, Chen L, Chen TM, Chin MC, Chong J, Crook BE, Czaplinska A, Dang CN, Datta S, Dee NR, Desaki AL, Desta T, Diep E, DolbeareTA, Donelan MJ, Dong HW, Dougherty JG, Duncan BJ, Ebbert AJ, Eichele G, Estin LK, Faber C, Facer BA, Fields R, Fischer SR, Fliss TP, Frensley C, Gates SN, Glattfelder KJ, Halverson KR, Hart MR, Hohmann JG, Howell MP, Jeung DP, Johnson RA, Karr PT, Kawal R, Kidney JM, Knapik RH, Kuan CL, Lake JH, Laramee AR, Larsen KD, Lau C, Lemon TA, Liang AJ, Liu Y, Luong LT, Michaels J, Morgan JJ, Morgan RJ, Mortrud MT, Mosqueda NF, Ng LL, Ng R, Orta GJ, Overly CC, Pak TH, Parry SE, Pathak SD, Pearson OC, Puchalski RB, Riley ZL, Rockett HR, Rowland SA, Royall JJ, Ruiz MJ, Sarno NR, Schaffnit K, Shapovalova NV, Sivisay T, Slaughterbeck CR, Smith SC, Smith KA, Smith BI, Sodt AJ, Stewart NN, Stumpf KR, Sunkin SM, Sutram M, Tam A, Teemer CD, Thaller C, Thompson CL, Varnam LR, Visel A, Whitlock RM, Wohnoutka PE, Wolkey CK, Wong VY, Wood M, Yaylaoglu MB, Young RC, Youngstrom BL, Yuan XF, Zhang B, Zwingman TA, Jones AR (2006) Genome-wide atlas of gene expression in the adult mouse brain. Nature 445: 168-176.

59. Lewis PA, Cookson MR (2012) Gene expression in the Parkinson’s disease brain. Brain Res Bull 88: 302-312.

60. Liang WS, Dunckley T, Beach TG, Grover A, Mastroeni D, Ramsey K, Caselli RJ, Kukull WA, McKeel D, Morris JC, Hulette CM, Schmechel D, Reiman EM, Rogers J,Stephan DA (2008) Altered neuronal gene expression in brain regions differentially affected by Alzheimer’s disease : a reference data set. Physiol Genomics 33: 240-256.

61. Lim S, Chun Y, Lee JS, Lee SJ (2016) Neuroinflammation in synucleinopathies. Brain Pathol 26: 404-409.

62. Lim SM, Katsifis A, Villemagne VL, Best R, Jones G, Saling M, Bradshaw J, Merory J, Woodward M, Hopwood M, Rowe CC (2009) The 18F-FDG PET cingulate island sign and comparison to 123I-beta-CIT SPECT for diagnosis of dementia with Lewy bodies. J Nucl Med 50: 1638-1645.

63. Marin R, Fabelo N, Martín V, Garcia-Esparcia P, Ferrer I, Quinto-Alemany D, Diaz M (2016) Anomalies occurring in lipid profiles and protein distribution in frontal cortex lipid rafts in dementia with Lewy bodies disclose neurochemical traits partially shared by Alzheimer's and Parkinson's diseases. Neurobiol Aging 49: 52-59.

64. McKeith I, Mintzer J, Aarsland D, Burn D, Chiu H, Cohen-Mansfield J, Dickson D, Dubois B, Duda JE, Feldman H, Gauthier S, Halliday G, Lawlor B, Lippa C, Lopez OL, Carlos Machado J, O'Brien J, Playfer J, Reid W; International Psychogeriatric Association Expert Meeting on DLB (2004) Dementia with Lewy bodies. Lancet Neurol 3: 19-28.

65. Milber JM, Noorigian JV, Morley JF, Petrovitch H, White L, Ross GW, Duda JE (2012) Lewy pathology is not the first sign of degeneration in vulnerable neurons in Parkinson disease. Neurology 79: 2307-2314.

66. Miller J, Woltjer RL, Goodenbour JM, Horvath S, Geschwind DH (2013) Genes and pathways underlying regional and cell type changes in Alzheimer’s disease. Genome Med 5: 48.

67. Mukaetova-Ladinska EB, Andras A, Milne J, Abdel-All Z, Borr I, Jaros E, Perry RH, Honer WG, Cleghorn A, Doherty J, McIntosh G, Perry EK, Kalaria RN, McKeith IG (2013) Synaptic proteins and choline acetyltransferase loss in visual cortex in dementia with Lewy bodies. J Neuropathol Exp Neurol 72: 53-60.

68. Navarro A, Boveris A (2009) Brain mitochondrial dysfunction and oxidative damage in Parkinson's disease. J Bioenerg Biomembr 41: 517-521.

69. Navarro A, Boveris A, Bández MJ, Sánchez-Pino MJ, Gómez C, Muntané G, Ferrer I (2009) Human brain cortex: mitochondrial oxidative damage and adaptive response in Parkinson disease and in dementia with Lewy bodies. Free Radic Biol Med 46: 1574-1580.

70. Nelson PT, Abner EL, Schmitt FA, Kryscio RJ, Jicha GA, Smith CD, Davis G, Poduska JW, Patel E, Mendiondo MS, Markesbery WR (2010) Modeling the association between 43 different clinical and pathological variables and the severity of cognitive impairment in a large autopsy cohort of elderly persons. Brain Pathol 20: 66-79.

71. Nelson PT, Kryscio RJ, Jicha GA, Abner EL, Schmitt FA, Xu LO, Cooper G, Smith CD, Markesbery WR (2009) Relative preservation of MMSE scores in autopsy-proven dementia with Lewy bodies. Neurology 73: 1127-1133.

72. Odunuga OO, Longshaw VM, Blatch GL (2004) Hop: more than an Hsp70/Hsp90 adaptor protein. BioEssays 26: 1058-1068.

73. Oldham MC, Konopka G, Iwamoto K, Langfelder P, Kato T, Horvath S, Geschwind DH (2009) Functional organization of the transcriptome in human brain. Nat Neurosci 11: 1271-1282.

74. Overk CR, Masliah E (2014) Pathogenesis of synaptic degeneration in Alzheimer's disease and Lewy body disease. Biochem Pharmacol 88: 508-516.

75. Parachikova A, Agadjanyan MG, Cribbs DH, Blurton-Jones M, Perreau V, Rogers J, Beach TG, Cotman CW (2007) Inflammatory changes parallel the early stages of Alzheimer disease. Neurobiol Aging 28: 1821-1833.

76. Parker WD, Parks JK, Swerdlow RH (2008) Complex I deficiency in Parkinson's disease frontal cortex. Brain Res 1189: 215-218.

77. Parkkinen L, Kauppinen T, Pirttilä T, Autere JM, Alafuzoff I (2005) α-synuclein pathology does not predict extrapyramidal symptoms or dementia. Ann Neurol 57: 82-91.

78. Parkkinen L, Pirttilä T, Alafuzoff I (2008) Applicability of current staging/categorization of alpha-synuclein pathology and their clinical relevance. Acta Neuropathol 115: 399-407.

79. Price DL, Rockenstein E, Ubhi K, Phung V, MacLean-Lewis N, Askay D, Cartier A, Spencer B, Patrick C, Desplats P, Ellisman MH, Masliah E (2010) Alterations in mGluR5 expression and signaling in Lewy body disease and in transgenic models of alpha-synucleinopathy--implications for excitotoxicity. PLoS One 5: e14020.

80. Ravid R, Ferrer I (2012) Brain banks as key part of biochemical and molecular studies on cerebral cortex involvement in Parkinson's disease. FEBS J 279: 1167-1176.

81. Ritchie ME, Phipson B, Wu D, Hu Y, Law CW, Shi W, Smyth GK (2015) Limma powers differential expression analyses for RNA-sequencing and microarray studies.Nucleic Acids Res 43: e47.

82. Roberts AJ, Kon T, Knight PJ, Sutoh K, Burgess SA (2013) Functions and mechanics of dynein motor proteins. Nat Rev Mol Cell Biol 14: 713-726.

83. Santiago JA, Potashkin JA (2014) A network approach to clinical intervention in neurodegenerative diseases. Trends Mol Med 20: 694-703.

84. Schulz-Schaeffer WJ (2010) The synaptic pathology of α-synuclein aggregation in dementia with Lewy bodies, Parkinson’s disease and Parkinson's disease dementia. Acta Neuropathol 120: 131-143.

85. Scott DA, Tabarean I, Tang Y, Cartier A, Masliah E, Roy S (2010) A pathologic cascade leading to synaptic dysfunction in alpha-synuclein-induced neurodegeneration. J Neurosci 30: 8083-8095.

86. Shannon P, Markiel A, Ozier O, Baliga NS, Wang JT, Ramage D, Amin N, Schwikowski B, Ideker T (2005) Cytoscape: a software environment for integrated models of biomolecular interaction networks. Am Assoc Cancer Res Educ B 13: 2498-2504.

87. Schneider JA, Arvanitakis Z, Yu L, Boyle PA, Leurgans SE, Bennette DA (2012) Cognitive impairment, decline and fluctuations in older community-dwelling subjects with Lewy bodies. Brain 135: 3005-3014.

88. Shepherd CE, Thiel E, McCann H, Harding AJ, Halliday GM (2000) Cortical inflammation in Alzheimer disease but not dementia with Lewy bodies. Arch Neurol 57: 817-822.

89. Shimada H, Hirano S, Shinotoh H, Aotsuka A, Sato K, Tanaka N, Ota T, Asahina M, Fukushi K, Kuwabara S, Hattori T, Suhara T, Irie T (2009) Mapping of brain acetylcholinesterase alterations in Lewy body disease by PET. Neurology 73: 273-278.

90. Streit WJ, Xue QS (2016) Microglia in dementia with Lewy bodies. Brain Behav Immun 55:191-201.

91. Thal DR, Rüb U, Orantes M, Braak H (2002) Phases of A beta-deposition in the human brain and its relevance for the development of AD. Neurology 58:1791-1800.

92. Thomas RR, Keeney PM, Bennett JP (2012) Impaired complex-I mitochondrial biogenesis in Parkinson disease frontal cortex. J Parkinsons Dis 2: 67-76.

93. Trentham DR, McMurray CH, Pogson CI (1969) The active chemical state of D-glyceraldehyde 3-phosphate in its reactions with D-glyceraldehyde 3-phosphate dehydrogenase, aldolase and triose phosphate isomerase. Biochem J 114: 19-24.

94. Walker DG, Lue LF, Serrano G, Adler CH, Caviness JN, Sue LI, Beach TG (2016) Altered expression patterns of inflammation-associated and trophic molecules in substantia nigra and striatum brain samples from Parkinson's disease, incidental Lewy body disease and normal control cases. Front Neurosci 9: 507.

Tables

Table 1: a) Main deregulated gene clusters in frontal cortex in iLBD. b) Main deregulated gene clusters in frontal cortex in DLB.

Table 2: a) Quantification of the expression of selected genes corresponding to axonema and taste receptors clusters in middle-aged (MA), iLBD, PD and DLB. Data are expressed as mean values ± SD; significant comparisons between groups are expressed by p values. Up-regulated and down-regulated genes are represented by different colours. b) Quantification of the expression of selected genes corresponding to RNA/DNA processing, chaperones and neurotransmitters, and synapses in middleaged (MA), iLBD, PD and DLB. Data are expressed as mean values ± SD; significant comparisons between groups are expressed by p values. Up-regulated and downregulated genes are represented by different colours. P-values have been adjusted using the BH method in each contrast and are indicated next to nominal p-values.

Supplementary tables

Supplementary Table 1: TaqMan probes used in the study, gene abbreviation, full name of the genes and references.

Supplementary Table 2: Number of DEGs for different thresholds for each comparison of iLBD, PD, DLB and middle aged individuals.

Supplementary Table 3: Gene ontology analysis comparing up- and down-regulated genes in the different categories.

Supplementary Table 4: Fifty top up-regulated and top down-regulated genes, frontal cortex area 8 in DLB.

Supplementary Table 5: Top 20 hub genes per modules.

Supplementary Table 6: Enrichment of modules in neuronal and glial cell markers, and commonalities with neurological diseases such as Alzheimer’s disease and autism.

Supplementary Table 7: Identification of enriched GO among genes in each module.

Figures legends

Figure 1: **a**) Heatmap representation of the enrichment scores of 1,914 genes having at least one group of samples with enrichment scores other than 0. MA: middle-aged, iLBD: incidental Lewy body disease, PD: Parkinson disease, DLB: dementia with Lewy bodies. **b**) Weighted gene co-expression network analysis of the frontal cortex transcriptome using 5,114 gene expression values of 28 assessed samples identifies 13 gene modules. Modules are labelled by colour and number (M1 to M13). Genes not assigned to any particular co-expression modules were labelled M0 or grey. Dendrogram obtained by hierarchical clustering of genes based on their topological overlap is shown at the top. Bottom rows indicate the correlation value of each gene expression and the spectrum of LBD pathology. Blue to red indicates negative to positive correlation values. None of our identified modules correlated with age.

Figure 2: **a**) Module eigengenes for each module by LB spectrum. **b**) Correlation values (univariate) and p-values for the relationship between each module eigengene and each LBD stage compared separately with MA or various control variables. P-values for LBD stages correspond to partial coefficients in the multivariate analysis. Colour code indicates the significance of the correlation. Seven modules significantly correlate with different stages of LBD.

Figure 3: Enrichment score (-log10 P-value) of genes in selected modules in previously published brain gene sets associated with cell types or brain regions. Module-brown (M6) is enriched in neuronal genes; module-tan (M5) is enriched in microglial genes; module-salmon (M6) has non-specific enrichment.

Figure 4: Putative sub-networks of protein-protein interactions. **a**) M6-tan module PPI sub-network showing that spleen tyrosine kinase (encoded by SYK) interacting with 16 partners is the gene with the highest degree of nucleation. **b**) M4-lightcyan module subnetwork showing high degree proteins such as CDK2, MSN and TP53. **c**) M9-salmon PPI sub-network shows a large connected node related to heat shock proteins encoded by STIP1, DNAJA1, DNAJB1, DNAJB4, HSPA5, HSAPA6, AHSA1 and HSPA1A, among others. **d**) M5-brown module contains a large PPI sub-network with several nodes including proteins encoded by YWHAB, GSK3B, PSMA3, ATP6V0D1, TPI1, ATP6V1A and SNCA, among others (circular network representation is shown in the small panel proteins ordered by degree, a zoom in the top degree proteins is shown in the larger panel).

List of abbreviations

AD Alzheimer's disease

AIF1 Allograft inflammatory factor 1

ATP6V1A ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A

CYCS Cytochrome c, somatic

DEG Differential expressed genes

DNAAF1 Dynein axonemal assembly factor 1

DNAH11 Dynein axonemal heavy chain 11

DNAH2 Dynein axonemal heavy chain 2

DNAH5 Dynein axonemal heavy chain 5

DNAH7 Dynein axonemal heavy chain 7

DNAH9 Dynein axonemal heavy chain 9

DNAI1 Dynein axonemal intermediate chain 1

DNAJA1 DnaJ (Hsp40) homolog, subfamily A, member 1

DNAJA4 DnaJ (Hsp40) homolog, subfamily A, member 4

DNAJB1 DnaJ (Hsp40) homolog, subfamily B, member 1

DNAJB4 DnaJ (Hsp40) homolog, subfamily B, member 4

DOT1L DOT1 like histone lysine methyltransferase

GABBR2 Gamma-aminobutyric acid (GABA) B receptor, 2

GABRA1 Gamma-aminobutyric acid (GABA) A receptor, alpha 1

GAD1 Glutamate decarboxylase 1 (brain, 67kDa)

GO Gene ontology

GRIN2A Glutamate receptor, ionotropic, N-methyl D-aspartate 2A

GRIN2B Glutamate receptor, ionotropic, N-methyl D-aspartate 2B

GSK3B Glycogen synthase kinase 3 beta

HSPA1A Heat shock 70kDa protein 1A

HSPA4 Heat shock 70kDa protein 4

HSPA5 Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)

HSPA6 Heat shock 70kDa protein 6 (HSP70B)

HSPD1 Heat shock 60kDa protein 1 (chaperonin)

HSPE1 MOB family member 4, phocein

iLBD Incidental LBD

iPD Incidental PD

KAT2A Lysine acetyltransferase 2A

LAPTM5 Lysosomal protein transmembrane 5

LB Lewy body

LBD Lewy body disease

MA Middle-aged individuals

NETO1 neuropilin (NRP) and tolloid (TLL)-like 1

NFT Neurofibrillary tangles

PAPOLA Poly(A) polymerase alpha

PD Parkinson's disease

PNPT1 Polyribonucleotide nucleotidyltransferase 1

PPI Protein-protein interaction

PSMA3 Proteasome (prosome, macropain) subunit, alpha type, 3

RAB3A RAB3A, member RAS oncogene family

RELA RELA proto-oncogene, NF-kB subunit

RIN RNA integritu number

rpDLB Rapid course DLB

RPH3A Rabphilin 3A homolog (mouse)

RT-qPCR Real time quantitative polymerase chain reaction

SNAP25 Synaptosomal-associated protein, 25kDa

STIP1 Stress-induced-phosphoprotein 1

STXBP1 Syntaxin binding protein 1

SYK Spleen associated tyrosine kinase

SYP Synaptophysin

SYT1 Synaptotagmin I

SYT13 Synaptotagmin XIII

SYT16 Synaptotagmin XVI

TAS2R10 Taste 2 receptor member 10

TAS2R13 Taste 2 receptor member 13

TAS2R14 Taste 2 receptor member 14

TAS2R5 Taste 2 receptor member 5

TAS2R50 Taste 2 receptor member 50

TPI1 Triosephosphate isomerase 1

WGCNA Weigted gene co-expression network analysis

YWHAB Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide

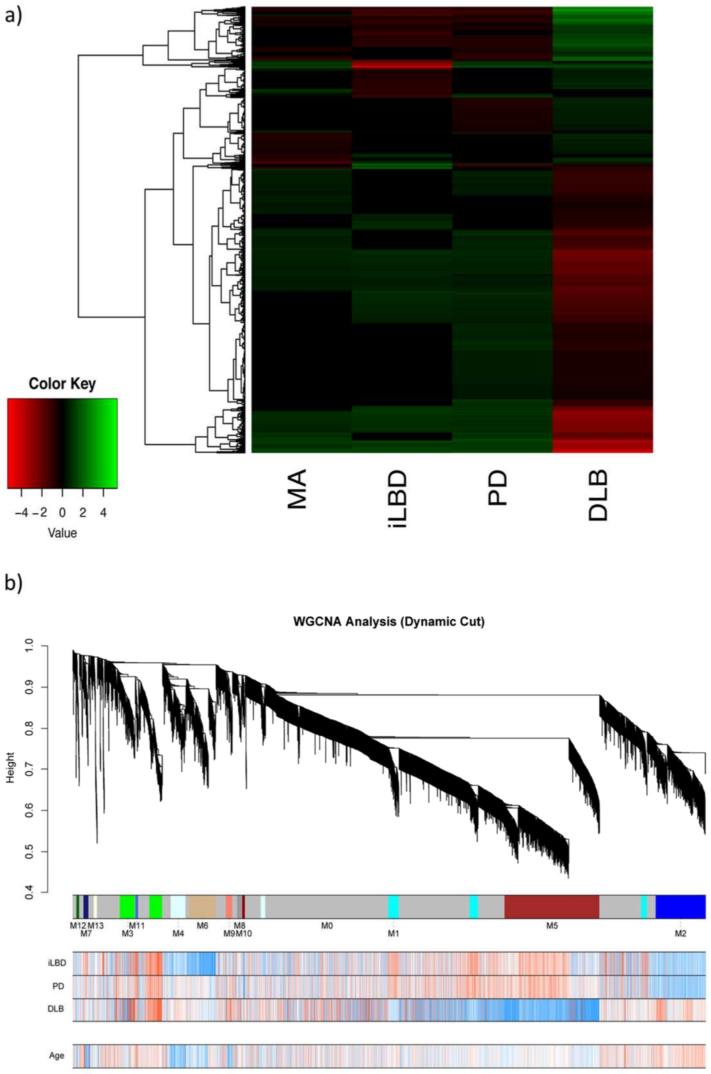
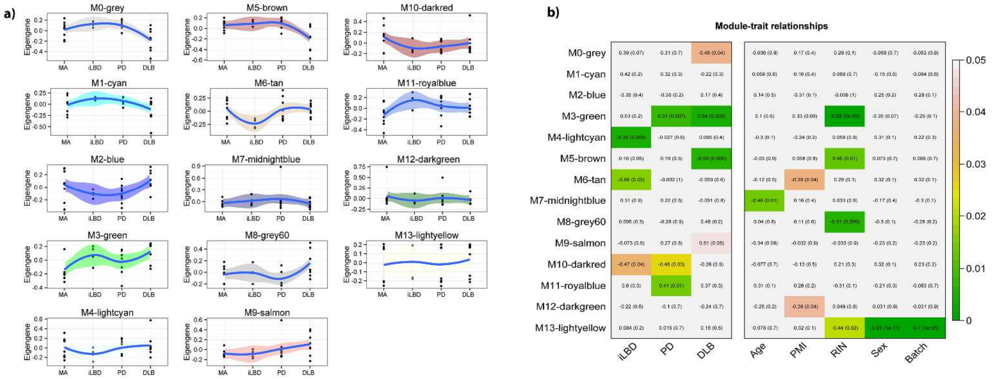


Figure 1: a) Heatmap representation of the enrichment scores of 1,914 genes having at least one group of samples with enrichment scores other than 0. MA: middle-aged, iLBD: incidental Lewy body disease, PD: Parkinson disease, DLB: dementia with Lewy bodies. b) Weighted gene co-expression network analysis of the frontal cortex transcriptome using 5,114 gene expression values of 28 assessed samples identifies 13 gene modules. Modules are labelled by colour and number (M1 to M13). Genes not assigned to any particular co-expression modules were labelled M0 or grey. Dendrogram obtained by hierarchical clustering of genes based on their topological overlap is shown at the top. Bottom rows indicate the correlation value of each gene expression and the spectrum of LBD pathology. Blue to red indicates negative to positive correlation values. None of our identified modules correlated with age.

119x180mm (300 x 300 DPI)



	iLBD	PD	DLB	Age	PMI	RIN	Sex	Batch
M0-grey	0.39 (0.07)	0.31 (0.7)	-0.48 (0.04)	-0.036 (0.9)	0.17 (0.4)	0.29 (0.1)	-0.068 (0.7)	-0.053 (0.8)
M1-cyan	0.42 (0.2)	0.32 (0.3)	-0.22 (0.3)	0.059 (0.8)	0.16 (0.4)	0.088 (0.7)	-0.15 (0.5)	-0.094 (0.6)
M2-blue	-0.35 (0.4)	-0.35 (0.2)	0.17 (0.4)	0.14 (0.5)	-0.31 (0.1)	-0.008 (1)	0.25 (0.2)	0.28 (0.1)
M3-green	0.53 (0.2)	0.31 (0.007)	0.64 (0.005)	0.1 (0.6)	0.33 (0.09)	-0.69 (5e-05)	-0.35 (0.07)	-0.29 (0.1)
M4-lightcyan	-0.38 (0.005)	-0.027 (0.6)	0.095 (0.4)	-0.3 (0.1)	-0.24 (0.2)	0.058 (0.8)	0.31 (0.1)	0.22 (0.3)
M5-brown	0.16 (0.05)	0.19 (0.5)	-0.59 (0.005)	-0.03 (0.9)	0.058 (0.8)	0.46 (0.01)	0.073 (0.7)	0.089 (0.7)
M6-tan	-0.66 (0.02)	-0.032 (1)	-0.059 (0.6)	-0.12 (0.5)	-0.39 (0.04)	0.29 (0.1)	0.32 (0.1)	0.32 (0.1)
M7-midnightblue	0.31 (0.9)	0.22 (0.5)	-0.091 (0.8)	-0.46 (0.01)	0.16 (0.4)	0.033 (0.9)	-0.17 (0.4)	-0.3 (0.1)
M8-grey60	0.095 (0.3)	-0.28 (0.9)	0.48 (0.2)	0.04 (0.8)	0.11 (0.6)	-0.51 (0.006)	-0.3 (0.1)	-0.28 (0.2)
M9-salmon	-0.073 (0.5)	0.27 (0.5)	0.51 (0.05)	-0.34 (0.08)	-0.032 (0.9)	-0.033 (0.9)	-0.23 (0.2)	-0.23 (0.2)
M10-darkred	-0.47 (0.04)	-0.48 (0.03)	-0.26 (0.5)	-0.077 (0.7)	-0.13 (0.5)	0.21 (0.3)	0.32 (0.1)	0.23 (0.2)
M11-royalblue	0.6 (0.3)	0.41 (0.01)	0.37 (0.3)	0.31 (0.1)	0.26 (0.2)	-0.31 (0.1)	-0.21 (0.3)	-0.083 (0.7)
M12-darkgreen	-0.22 (0.6)	-0.1 (0.7)	-0.24 (0.7)	-0.25 (0.2)	-0.39 (0.04)	0.049 (0.8)	0.031 (0.9)	-0.031 (0.9)
M13-lightyellow	0.084 (0.2)	0.015 (0.7)	0.16 (0.5)	-0.078 (0.7)	0.32 (0.1)	-0.44 (0.02)	0.91 (1e-11)	0.7 (3e-05)

Figure 2: a) Module eigengenes for each module by LB spectrum. b) Correlation values (univariate) and p-values for the relationship between each module eigengene and each LBD stage compared separately with MA or various control variables. P-values for LBD stages correspond to partial coefficients in the multivariate analysis. Colour code indicates the significance of the correlation. Seven modules significantly correlate with different stages of LBD.

549x218mm (300 x 300 DPI)

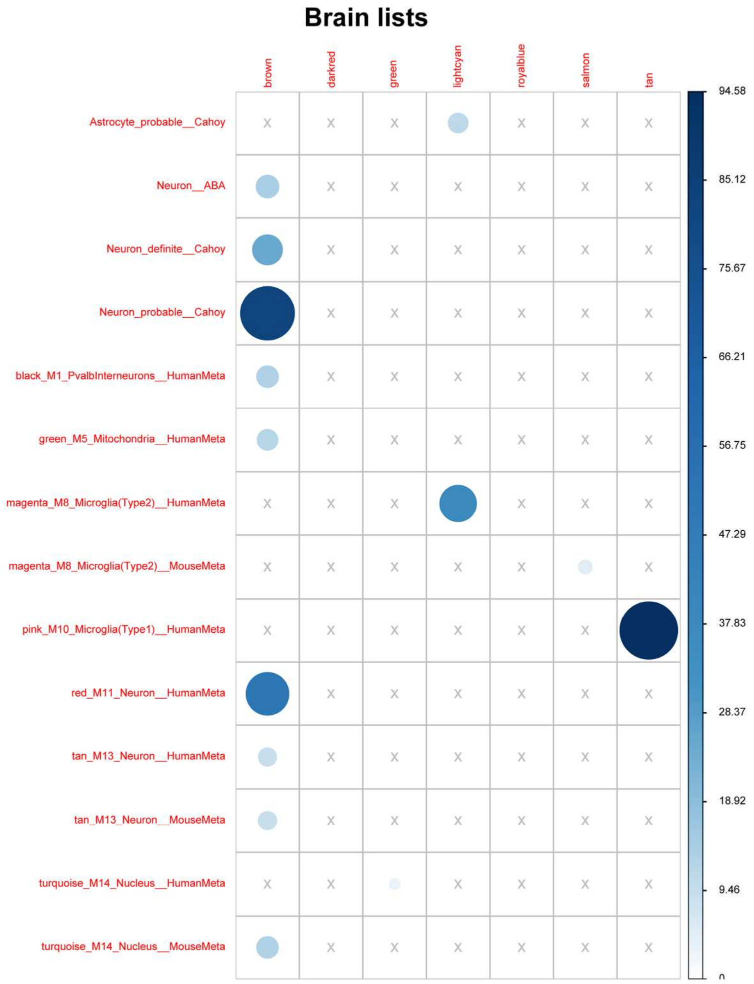


Figure 3: Enrichment score (-log10 P-value) of genes in selected modules in previously published brain gene sets associated with cell types or brain regions. Module-brown (M6) is enriched in neuronal genes; module-tan (M5) is enriched in microglial genes; module-salmon (M6) has non-specific enrichment.

197x205mm (300 x 300 DPI)

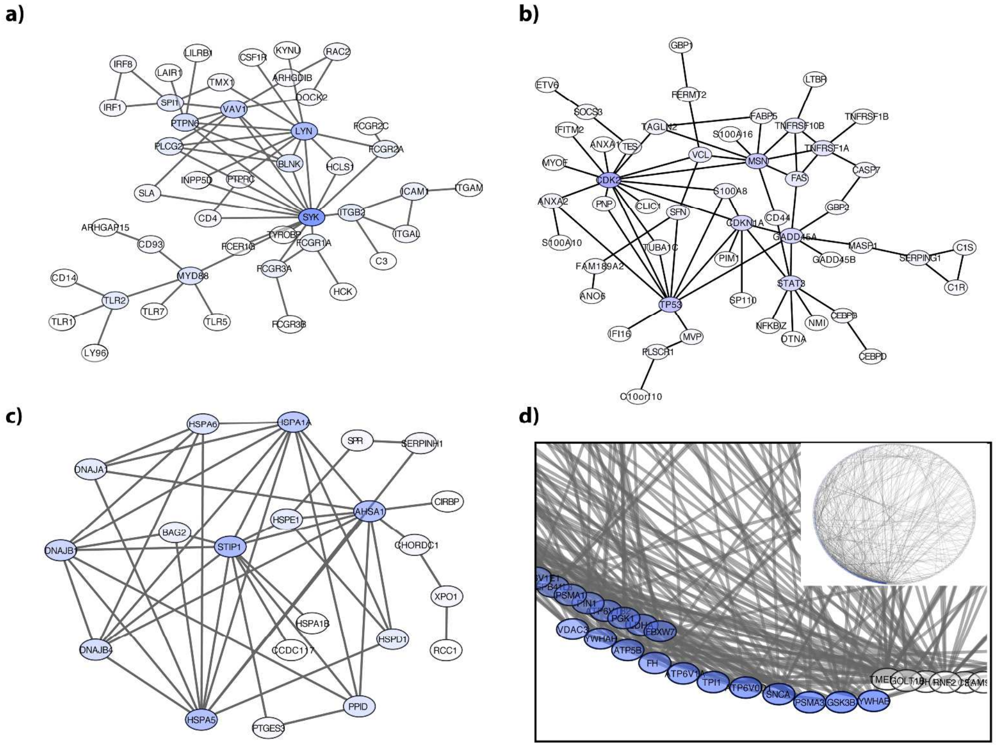


Figure 4: Putative sub-networks of protein-protein interactions. a) M6-tan module PPI sub-network showing that spleen tyrosine kinase (encoded by SYK) interacting with 16 partners is the gene with the highest degree of nucleation. b) M4-lightcyan module subnetwork showing high degree proteins such as CDK2, MSN and TP53. c) M9-salmon PPI sub-network shows a large connected node related to heat shock proteins encoded by STIP1, DNAJA1, DNAJB1, DNAJB4, HSPA5, HSAPA6, AHSA1 and HSPA1A, among others. d) M5-brown module contains a large PPI sub-network with several nodes including proteins encoded by YWHAB, GSK3B, PSMA3, ATP6V0D1, TPI1, ATP6V1A and SNCA, among others (circular network representation is shown in the small panel proteins ordered by degree, a zoom in the top degree proteins is shown in the larger panel).

349x261mm (300 x 300 DPI)

Table 1: a) Main deregulated gene clusters in frontal cortex in iLBD. **b)** Main deregulated gene clusters in frontal cortex in DLB

a)

Cluster	Gene names	Count	Size	Odds Ratio	p-value	Deregulation
Adaptive immune response	C3AR1 C3 C1QC C1QB INPP5D PTPN6 ADA FCER1G CTSC TGFB1	10	58	12.64	0.00	Down
Antigen processing and presentation	SEC23A RAB3B PSMD8 PSMC2 PSMB2 ACTR1B LGMN RAB7A PSMB3 RAB3C DCTN6 AP1S1 PSMD12 DCTN2 DCTN3 PSMA5 AP2M1 PSMB6 PSMC4 PSMA3 PSMA4 DYNC1I1 KIF3A AP1M1	24	65	2.85	0.00	Down
Axonemal dynein complex assembly	LRRC6	1	2	353.08	0.01	Up
Cell activation involved in immune response	APBB1IP TYROBP VAMP8 ADA LCP1 FCER1G HLA-DMB TGFB1	8	52	10.72	0.00	Down
Detection of chemical stimulus involved in sensory perception of bitter taste	TAS2R4 TAS2R14	2	5	256.67	0.00	Up
Granulocyte activation	TYROBP FCER1G	2	7	21.94	0.01	Down
Innate immune response	CSF1R HLA-DPB1 AIF1 C3 TYROBP C1QC C1QB HLA-DPA1 TREM2 TRIM22 ITGB2 PTPN6 CYBB FCER1G RPS6KA1 VSIG4 TGFB1 CXCL16	18	277	4.53	0.00	Down
Lymphocyte activation involved in immune response	APBB1IP ADA LCP1 FCER1G HLA-DMB TGFB1	6	31	13.83	0.00	Down
Mononuclear cell proliferation	HLA-DPB1 AIF1 LST1 HLA-DPA1 INPP5D ITGB2 PTPN6 ADA HLA-DMB VSIG4 TGFB1	11	54	15.77	0.00	Down
Myeloid dendritic cell activation	TGFBR2 CD37 TGFB1	3	8	33.34	0.00	Down
Positive regulation of mast cell activation	VAMP8 FCER1G	2	7	21.94	0.01	Down
Regulation of B cell mediated immunity	C3 PTPN6 FCER1G TGFB1	4	8	56.34	0.00	Down
Regulation of immunoglobulin production	CD37 TGFB1	2	8	18.28	0.01	Down
T cell activation involved in immune response	APBB1IP LCP1 FCER1G HLA-DMB	4	13	25.01	0.00	Down

b)

Cluster	Gene names	Count	Size	Odds Ratio	p-value	Deregulation
Antigen processing and presentation	SEC23A RAB3B PSMD8 PSMC2 PSMB2 ACTR1B LGMN RAB7A PSMB3 RAB3C DCTN6 AP1S1 PSMD12 DCTN2 DCTN3 PSMA5 AP2M1 PSMB6 PSMC4 PSMA3 PSMA4 DYNC1I1 KIF3A AP1M1	24	65	2.85	0.00	Down
Antigen processing and presentation of exogenous peptide antigen via MHC class II	SEC23A ACTR1B LGMN RAB7A DCTN6 AP1S1 DCTN2 DCTN3 AP2M1 DYNC1I1 KIF3A AP1M1	12	29	3.40	0.00	Down
Apoptotic mitochondrial changes	SLC25A4 YWHAZ MLLT11 DNM1L PARK2 FAM162A YWHAB MAPK9 BLOC1S2 YWHAG GSK3B GGCT OPA1 PIM2	14	40	2.60	0.01	Down
ATP hydrolysis coupled proton transport	ATP6V1F ATP5B ATP6V1E1 ATP6AP1 ATP6V1B2 ATP5G1 ATP6V0D1 ATP6V1C1 ATP6V1A ATP1A1 ATP6V0A1 ATP1A3 ATP6V1H ATP5A1	14	17	22.66	0.00	Down
ATP metabolic process	COX8A NDUFB5 ATP5B OLA1 NDUFA5 ATP6V1B2 ATP5G1 ENTPD5 DLD HTR2A DNM1L PRKAG1 ATP6V1A CYCS ENO2 NDUFA9 UQCRC1 PGK1 UQCRC2 ATP6V0A1 BPGM HK1 NDUFS3 GBAS NDUFS4 NDUFV2 ATP5H PPP2R5D NDUFAB1 ATP5A1	30	77	3.13	0.00	Down
Cell proliferation	AKR1C2 PRKX GJA1 NUPR1 P2RX7 FGF17 TYK2 TOB2 HDAC4 MSX1 RXRA IKBKB FLCN PTCH1 YAP1 CD151 NACC2 LRP2 ID4 TNS3 KAT2A CDC14A GPER1 FOXO1 FOXC1 RELA EPS8	27	536	2.04	0.00	Up
Coenzyme metabolic process	IDH3G PNPO MDH2 PDHB IDH3B ACLY RFK AASDHPPT ENTPD5 DLD HTR2A DLAT PRKAG1 ENO2 NMNAT2 MDH1 NDUFA9 SLC25A32 PDP1 PGK1 ELOVL6 ELOVL4 BPGM FAR2 HK1 PTS PDK3 ACSL4 SUCLA2 KCNAB2 PPP2R5D MVK MAT2B	33	113	2.01	0.00	Down
Covalent chromatin modification	EYA2 RBM14 HDAC4 FLCN NACC2 KAT2A DOT1L	7	80	3.41	0.01	Up
Developmental process	PRELP KLF15 PNPT1 AKR1C2 PRKX LRP4 GJA1 WWC3 SLC5A3 NUPR1 P2RX7 FGF17 EYA2 TYK2 AK4 CPQ TOB2 HDAC4 CAPN2 ADGRV1 MSX1 MRAS PPP2R1B RXRA IKBKB SASH1 ANKRD11 CDC42EP4 ZIC2 FLCN PTCH1 PCID2 MT1G YAP1 S100A1 ID3 CA2 DNAJB6 GNA12 ROCK1 LRP2 RAMP1 PPP1R13L SPR FRYL ARAP1 ID4 HIF3A SRGAP1 SLC39A12 VCAN TNS3 KAT2A CDC14A GPER1 FOXO1 FOXC1 MAN2A1 EHD2 PI16 RELA EPS8	62	1671	1.65	0.00	Up
Electron transport chain	COX8A NDUFB5 ATP5B NDUFA5 ATP5G1 ALDH5A1 DLD CYCS NDUFA9 UQCRC1 SLC25A14 UQCRFS1 UQCRC2 SLC25A12 NDUFS3 NDUFS4 NDUFV2 ATP5H NDUFAB1 ATP5A1	20	43	4.23	0.00	Down
Exocytosis	VPS33B TUBA4A SNX4 CDK5 NAPA RAB3B RPH3A PLCB1 PFN2 SYT5 ATP6AP1 PAK1 CHP1 SCAMP1 SCFD2 RAB7A RAB3C RASGRP1 SCAMP5 NSF SNAP25 HABP4 RAB3A VPS33A KIT VAMP1 PPIA VSNL1 STXBP1 RAB27B VPS4B SYT13 CRHBP VAMP2 RALB BLOC1S6 SYT16 CDK5R2 SYT1 DOC2A ARHGAP44 PPP3CB	42	160	1.74	0.00	Down
Gluconeogenesis	GOT1 MDH2 RBP4 SLC35B4 ENO2 MDH1 PRKACA PGK1 G6PC3 BPGM SLC25A12 GOT2	12	31	3.04	0.00	Down
Histone modification	EYA2 RBM14 HDAC4 FLCN NACC2 KAT2A DOT1L	7	80	3.41	0.01	Up
Innate immune response activating cell surface receptor signaling pathway	PAK1 PSMD8 PSMC2 PSMB2 PSMB3 PRKACA PSMD12 PSMA5 PSMB6 UBE2N PSMC4 PSMA3 PSMA4 TAB3 PPP3CB	15	44	2.50	0.01	Down
miRNA metabolic process	PNPT1 RELA	2	4	34.69	0.00	Up

Mitochondrial electron transport, NADH to ubiquinone	NDUFB5 NDUFA5 DLD NDUFA9 NDUFS3 NDUFS4 NDUFV2 NDUFAB1	8	16	4.81	0.00	Down
Mitochondrial translation	MRPL15 MRPL30 MRPL37 HARS MTFMT LRPPRC CHCHD1 MRPL45 MPV17L2 MRPS21 MRPL42	11	27	3.31	0.00	Down
Mitochondrial transport	TOMM20 VPS11 MPC2 ATP5B YWHAZ PSMD8 ATP5G1 TIMM17A HAX1 PARK2 TOMM34 TOMM70A TOMM22 SLC25A32 BAG4 NRG1 SLC25A14 YWHAB MAPK9 UGCG BLOC1S2 YWHAG DNAJC19 SLC25A12 MTX3 GSK3B MICU1 KIF1BP ATP5H ATP5A1	30	104	1.97	0.00	Down
mRNA polyadenylation	PNPT1 PAPOLA	2	4	34.69	0.00	Up
NADH metabolic process	IDH3G MDH2 IDH3B ENO2 MDH1 PGK1 HK1 PPP2R5D	8	18	3.85	0.01	Down
Neuron-neuron synaptic transmission	CDK5 NAPA RAB3B PAK1 CHRNB2 CAMK4 CACNB4 GABRA1 HTR2A GRIN2A SLC6A1 PARK2 PRKACA GABRG2 STXBP1 GLRA2 MEF2C GRIA3 CRHBP GRIN3A SYT1 DNM1 PNKD	23	80	1.95	0.01	Down
Neurotransmitter transport	SLC32A1 CDK5 GAD1 SV2C GAD2 NAPA RAB3B RPH3A PFN2 SYT5 PAK1 ALDH5A1 SV2A NRXN3 PPT1 SLC6A1 SLC6A17 RAB3C PARK2 SNAP25 RAB3A ATP2A2 STXBP1 SLC38A1 SYT13 MEF2C VAMP2 BLOC1S6 SYT16 SYT1 DOC2A SV2B ICA1	33	112	2.04	0.00	Down
Nucleobase-containing compound metabolic process	KLF15 PNPT1 ZNF471 AHNAK GJA1 PAN2 WWC3 NUPR1 P2RX7 EYA2 RBM14 AK4 HDAC4 SAFB2 MSX1 RBMS2 RXRA IKBKB TRIM52 ZIC2 FLCN RAD52 IFI27 PTCH1 PCID2 YAP1 S100A1 ID3 SNRNP48 ZFHX2 DNAJB6 NACC2 CRY1 RAMP1 PPP1R13L FRYL ID4 HIF3A PAPOLA KAT2A RFX2 ZNF347 GPER1 TCP10L FOXO1 POLN TOP3B FOXC1 RELA GABPB2 DOT1L RBM4B MICAL3	53	1235	1.94	0.00	Up
Phagosome maturation	ATP6V1F ATP6V1E1 ATP6V1B2 ATP6V0D1 ATP6V1C1 RAB7A ATP6V1A ATP6V0A1 ATP6V1H ATP6V1D	10	18	6.03	0.00	Down
Proteasome-mediated ubiquitin-dependent protein catabolic process	ERLEC1 USP5 KCTD13 PSMD8 PSMC2 PSMB2 USP11 PSMB3 PARK2 USP10 UBXN11 FBXO9 PRICKLE1 FBXL2 PSMD12 PLK2 RNF185 PSMA5 PSMB6 PSMC4 UCHL1 UBE2W PSMA3 GSK3B PSMA4 GLMN BBS7 RNF14 RNF4 NEDD4L	30	99	2.12	0.00	Down
Protein K11-linked ubiquitination	UBE2E2 PARK2 UBE2W UBE2T RNF4	5	7	11.99	0.00	Down
Protein K6-linked ubiquitination	PARK2 UBE2T RNF4	3	3	Inf	0.01	Down
Protein monoubiquitination	PARK2 FBXL2 UBE2W TRIM37 RNF2 UBE2T	6	11	5.76	0.01	Down
Protein ubiquitination involved in ubiquitin-dependent protein catabolic process	PSMD8 PSMC2 PSMB2 PSMB3 PARK2 PSMD12 PSMA5 PSMB6 PSMC4 PSMA3 PSMA4 RNF14 NEDD4L	13	37	2.61	0.01	Down
Proton transport	COX8A ATP6V1F ATP5B ATP6V1E1 SLC9A7 ATP6AP1 ATP6V1B2 ATP5G1 ATP6V0D1 CHP1 ATP6V1C1 ATP6V1A SLC9A6 COX7A2 UQCRC1 SLC25A14 ATP1A1 UQCRFS1 SLC2A13 ATP6V0A1 ATP1A3 ATP6V1H ATP5H SLC9B2 ATP6V1D ATP5A1	26	59	3.86	0.00	Down
Purine nucleoside metabolic process	DGUOK COX8A NDUFB5 ATP5B PRPS1 OLA1 MPP1 NDUFA5 ATP6V1B2 HPRT1 ATP5G1 ACLY ENTPD5 DLD HTR2A DNM1L PRKAG1 ATP6V1A CYCS ENO2 NDUFA9 UQCRC1 DLG3 PGK1 UQCRC2 ATP6V0A1 BPGM HK1 NDUFS3 GBAS NDUFS4 NDUFV2 ATP5H PPP2R5D NDUFAB1 MAT2B ATP5A1	37	111	2.46	0.00	Down
Regulation of cell cycle	PNPT1 NUPR1 RBM14 KLHL21 MSX1 FLCN PTCH1 PCID2 ID3 NACC2 CRY1 CENPJ CDC14A GPER1 FOXC1 CTDSP2 CAB39L DOT1L	18	259	2.82	0.00	Up
Regulation of gene expression	KLF15 ZNF471 AHNAK GJA1 WWC3 NUPR1 P2RX7 EYA2 RBM14 TOB2 HDAC4 SAFB2 MSX1 RXRA IKBKB TRIM52 ZIC2 FLCN IFI27 PTCH1 PCID2 YAP1 S100A1 ID3 ZFHX2 DNAJB6 NACC2 CRY1 PPP1R13L FRYL ID4 HIF3A PAPOLA KAT2A RFX2 ZNF347 GPER1 TCP10L FOXO1 FOXC1 RELA GABPB2 DOT1L RBM4B MICAL3	45	908	2.24	0.00	Up

Regulation of macromolecule biosynthetic process	KLF15 ZNF471 GJA1 WWC3 NUPR1 MARCH8 EYA2 RBM14 HDAC4 SAFB2 MSX1 RXRA IKBKB TRIM52 ZIC2 FLCN IFI27 PTCH1 PCID2 YAP1 S100A1 ID3 ZFHX2 DNAJB6 NACC2 CRY1 RAMP1 PPP1R13L FRYL ID4 HIF3A KAT2A RFX2 ZNF347 GPER1 TCP10L FOXO1 FOXC1 RELA GABPB2 DOT1L RBM4B MICAL3	43	863	2.23	0.00	Up
Regulation of mitochondrion organization	VPS11 BECN1 YWHAZ PSMD8 MLLT11 DDHD2 DNM1L HAX1 PARK2 FAM162A BAG4 NRG1 YWHAB UGCG LRPPRC YWHAG HK1 GSK3B OPA1 MPV17L2	20	66	2.10	0.01	Down
Regulation of ubiquitin-protein transferase activity	PSMD8 PSMC2 PSMB2 PSMB3 PIN1 PSMD12 PSMA5 PSMB6 UBE2N PSMC4 PSMA3 DYNC1LI1 LCMT1 PSMA4	14	40	2.60	0.01	Down
Synaptic transmission	SLC32A1 CDK5 GAD1 NCALD CALB1 GAD2 NAPA RAB3B GNG3 RPH3A PLCB1 PFN2 SYT5 PAK1 KCND2 ASIC2 ALDH5A1 GABRA3 HCN1 NRXN3 LRRTM1 CHRNB2 CAMK4 CACNB4 PPT1 GABRA1 ARHGEF9 HTR2A GRIN2A SLC6A1 KCNAB1 RAB3C PARK2 CACNG3 SEZ6 PRKACA SST NSF SNAP25 GABRA4 GABRG2 KCNC2 RAB3A LRRTM2 KIT PLK2 DLG3 GRIN2B RASGRF1 HTR4 ATP2A2 GABRA5 STXBP1 SNCB SLC38A1 AP2M1 SYT13 GLRA2 MEF2C GRIA3 CRHBP VAMP2 YWHAG GRIN3A FGF12 KCNQ5 NETO1 NCDN BLOC1S6 SYT16 CACNB1 SYT1 DOC2A CHRM4 GABRB3 KCNH7 GNAL KCNAB2 GABBR2 CACNG2 DNM1 PCDH8 PANX1 AKAP5 PNKD PPP3CB SYP FGF14	88	390	1.44	0.00	Down
Synaptic transmission, dopaminergic	CDK5 RAB3B CHRNB2 PARK2 CRHBP PNKD	6	12	4.80	0.01	Down
Tissue development	KLF15 AKR1C2 PRKX LRP4 GJA1 NUPR1 P2RX7 EYA2 CPQ HDAC4 MSX1 RXRA IKBKB ZIC2 PTCH1 YAP1 ID3 CA2 ROCK1 PPP1R13L KAT2A FOXC1 MAN2A1 PI16 RELA	25	493	2.04	0.00	Up
Transcription from RNA polymerase II promoter	KLF15 WWC3 RBM14 HDAC4 MSX1 RXRA IKBKB FLCN IFI27 PTCH1 YAP1 S100A1 ID3 NACC2 CRY1 PPP1R13L ID4 HIF3A PAPOLA KAT2A RFX2 GPER1 TCP10L FOXO1 FOXC1 RELA GABPB2 MICAL3	28	461	2.57	0.00	Up
Transcription, DNA-templated	KLF15 ZNF471 WWC3 NUPR1 EYA2 RBM14 HDAC4 SAFB2 MSX1 RXRA IKBKB TRIM52 ZIC2 FLCN IFI27 PTCH1 PCID2 YAP1 S100A1 ID3 ZFHX2 DNAJB6 NACC2 CRY1 PPP1R13L FRYL ID4 HIF3A PAPOLA KAT2A RFX2 ZNF347 GPER1 TCP10L FOXO1 FOXC1 RELA GABPB2 DOT1L MICAL3	40	785	2.24	0.00	Up
Ubiquitin-dependent protein catabolic process	ERLEC1 USP5 KCTD13 PSMD8 PSMC2 PSMB2 USP11 PSMB3 PARK2 NDFIP1 USP10 UBXN11 FBXO9 PRICKLE1 FBXL2 PSMD12 PLK2 RLIM RNF185 VPS25 PSMA5 VPS4B PSMB6 UBE2N PSMC4 COPS3 UCHL1 UBE2W PSMA3 GSK3B PSMA4 GLMN BBS7 RNF14 RNF4 UCHL5 NEDD4L	37	123	2.11	0.00	Down
Vesicle docking	VPS33B RAB3B SCFD2 RAB3C NSF SNAP25 RAB3A VPS33A STXBP1 RAB27B RALB STX12 BLOC1S6	13	28	4.19	0.00	Down
Vesicle organization	VPS11 VPS33B SNX4 SEC23A COPG1 NSG1 RAB7A SNAP25 COPZ1 RAB3A VAMP1 PRKCI PTPRN STXBP1 VPS4B SNX10 BLOC1S2 VAMP2 STX12 VTA1 BLOC1S6 HMP19 AP1M1 SYP	24	79	2.12	0.00	Down

Table 2: a) Quantification of the expression of selected genes corresponding to axonema and taste receptors clusters in middle-aged (MA), iLBD, PD abd DLB. **b)** Quantification of the expression of selected genes corresponding to RNA/DNA processing, chaperones and neurotransmitters and synapses in middle-aged (MA), iLBD, PD and DLB.

a)

						P-VALUE		P-VALUE		P-VALUE	
	Probes	**MA**	**iLBD**	**PD**	**DLB**	**MA vs iLBD**	**Adjusted**	**MA vs PD**	**Adjusted**	**MA vs DLB**	**Adjusted**
Axonema	*DNAAF1*	1.04 ± 0.31	2.18 ± 0.72	2.06 ± 1.03	1.04 ± 0.36	0,000481	0,013524	0,005583	0,078162	0,987973	0,987973
	DNAH11	1.16 ± 0.57	3.17 ± 1.94	1.96 ± 0.51	3.27 ± 2.43	0,005601	0,039207	0,003889	0,078162	0,011763	0,043544
	DNAH2	1.07 ± 0.41	2.03 ± 0.97	2.40 ± 1.50	1.05 ± 0.38	0,012770	0,061973	0,010576	0,085253	0,899477	0,944451
	DNAH5	1.08 ± 0.44	1.76 ± 0.89	1.69 ± 0.83	1.05 ± 0.51	0,064296	0,245494	0,060820	0,196495	0,886887	0,944451
	DNAH7	1.08 ± 0.42	1.84 ± 0.69	1.35 ± 0.51	1.67 ± 0.45	0,016352	0,068678	0,227373	0,471895	0,007938	0,039284
	DNAH9	1.16 ± 0.63	2.39 ± 2.25	2.36 ± 1.25	1.67 ± 0.56	0,105147	0,339706	0,012179	0,085253	0,084009	0,147016
	DNAI1	1.07 ± 0.43	2.13 ± 0.32	3.09 ± 2.22	2.96 ± 1.44	0,000644	0,013524	0,008326	0,085253	0,000592	0,021154
Taste receptors	*TAS2R4*	1.03 ± 0.27	1.48 ± 1.12	1.33 ± 0.80	1.82 ± 0.78	0,203630	0,503086	0,247183	0,471895	0,004187	0,035171
	TAS2R5	1.03 ± 0.25	0.61 ± 0.33	1.14 ± 0.67	2.25 ± 1.03	0,013280	0,061973	0,639661	0,814114	0,001261	0,021154
	TAS2R14	1.15 ± 0.57	0.89 ± 0.54	2.44 ± 2.31	2.51 ± 1.59	0,427225	0,690133	0,077225	0,231675	0,012441	0,043544
	TAS2R50	1.08 ± 0.40	0.68 ± 0.42	0.65 ± 0.65	1.54 ± 1.15	0,091428	0,319998	0,089294	0,250023	0,229848	0,321787
	TAS2R10	1.13 ± 0.50	1.49 ± 1.09	4.50 ± 3.33	1.68 ± 0.64	0,371381	0,628649	0,002611	0,078162	0,038324	0,080480
	TAS2R13	1.11 ± 0.49	7.27 ± 5.99	0.99 ± 0.50	1.63 ± 0.62	0,002092	0,021966	0,625557	0,814114	0,042350	0,080850

🟩 dow nregulation
🟥 upregulation

b)

						P-VALUE		P-VALUE		P-VALUE	
	Probes	MA	iLBD	PD	DLB	MA vs iLBD	Adjusted	MA vs PD	Adjusted	MA vs DLB	Adjusted
RNA/DNA	*KAT2A*	1.08 ± 0.39	1.38 ± 0.80	1.68 ± 0.75	1.65 ± 1.22	0,318894	0,608798	🟥 0,032546	🟥 0,113911	0,162525	0,252817
	PNPT1	1.03 ± 0.26	1.73 ± 0.45	1.63 ± 0.74	2.18 ± 0.99	🟥 0,001300	🟥 0,018200	🟥 0,020982	🟥 0,106943	🟥 0,001511	🟥 0,021154
	PAPOLA	1.01 ± 0.18	1.02 ± 0.55	1.01 ± 0.33	1.52 ± 0.68	0,966720	0,990299	0,987272	0,997676	🟥 0,029792	🟥 0,069238
	RELA	1.01 ± 0.14	1.42 ± 0.39	1.62 ± 0.79	2.39 ± 1.84	🟥 0,009412	🟥 0,056472	🟥 0,027832	🟥 0,106943	🟥 0,029333	🟥 0,069238
	DOT1L	1.01 ± 0.16	1.28 ± 0.62	1.24 ± 0.60	1.34 ± 0.48	0,179901	0,472240	0,241060	0,471895	🟥 0,046556	🟥 0,085015
Chaperones	*DNAJA1*	1.02 ± 0.19	1.24 ± 0.58	1.32 ± 0.36	1.51 ± 0.75	0,249723	0,525382	🟥 0,027383	🟥 0,106943	🟥 0,041181	🟥 0,080850
	DNAJA4	1.28 ± 0.76	1.62 ± 1.15	1.75 ± 0.83	2.53 ± 1.19	0,479652	0,719478	0,199588	0,471895	🟥 0,008306	🟥 0,039284
	DNAJB1	1.21 ± 0.65	1.13 ± 0.58	1.14 ± 0.54	2.47 ± 0.54	0,827989	0,921038	0,822303	0,933425	🟥 0,020325	🟥 0,056910
	DNAJB4	1.21 ± 0.73	1.32 ± 0.70	1.13 ± 0.28	1.64 ± 0.82	0,788308	0,921038	0,776413	0,905815	0,223143	0,321787
	HSPA1A	1.06 ± 0.40	1.16 ± 0.55	1.28 ± 0.88	1.63 ± 1.55	0,727662	0,901719	0,490696	0,775885	0,283092	0,349702
	HSPA4	1.01 ± 0.12	1.05 ± 0.37	1.34 ± 0.42	1.63 ± 0.72	0,727987	0,901719	🟥 0,016296	🟥 0,097776	🟥 0,007965	🟥 0,039284
	HSPA5	1.06 ± 0.38	0.84 ± 0.29	1.70 ± 0.78	1.48 ± 0.82	0,270249	0,540498	🟥 0,028009	🟥 0,106943	0,143620	0,232002
	HSPA6	1.06 ± 0.39	0.86 ± 0.29	1.24 ± 0.91	1.63 ± 0.47	0,374196	0,628649	0,557809	0,780933	🟥 0,017922	🟥 0,056910
	HSPD1	1.02 ± 0.22	1.01 ± 0.66	1.17 ± 0.46	1.98 ± 1.28	0,950284	0,990299	0,324922	0,568614	🟥 0,018989	🟥 0,056910
	HSPE1	1.01 ± 0.13	1.04 ± 0.47	1.25 ± 0.50	1.04 ± 0.29	0,827808	0,921038	0,114919	0,301662	0,721566	0,819075
Neurotransmitters and synapses	*GABBR2*	1.05 ± 0.32	1.15 ± 0.48	1.05 ± 0.46	0.64 ± 0.32	0,616222	0,862711	0,281410	0,513879	🟩 0,012003	🟩 0,043544
	GABRA1	1.07 ± 0.40	0.88 ± 0.56	1.05 ± 0.52	0.60 ± 0.50	0,451273	0,701980	0,913177	0,958836	🟩 0,031322	🟩 0,069238
	GAD1	1.08 ± 0.43	0.73 ± 0.45	1.08 ± 0.45	0.50 ± 0.34	0,161648	0,452614	0,997676	0,997676	🟩 0,004059	🟩 0,035171
	GRIN2A	1.04 ± 0.28	1.04 ± 0.43	1.18 ± 0.45	1.14 ± 0.51	0,999447	0,999447	0,393711	0,661434	0,560841	0,654315
	GRIN2B	1.03 ± 0.27	0.99 ± 0.81	0.93 ± 0.41	1.19 ± 0.56	0,869824	0,936734	0,534280	0,775885	0,409171	0,491005
	NETO1	1.05 ± 0.32	0.47 ± 0.14	1.12 ± 0.75	0.64 ± 0.44	🟩 0,005157	🟩 0,039207	0,771798	0,905815	🟩 0,027200	🟩 0,069238
	RAB3A	1.03 ± 0.25	1.09 ± 0.04	1.14 ± 0.48	0.79 ± 0.53	0,636911	0,862912	0,535730	0,775885	0,218554	0,321787
	RPH3A	1.03 ± 0.25	1.10 ± 0.55	1.13 ± 0.53	0.78 ± 0.41	0,729963	0,901719	0,594324	0,805213	0,117159	0,196827
	SNAP25	1.02 ± 0.22	1.06 ± 0.42	1.23 ± 0.49	0.85 ± 0.43	0,833320	0,921038	0,220065	0,471895	0,263212	0,334997
	STXBP1	1.02 ± 0.20	1.12 ± 0.46	1.22 ± 0.49	0.86 ± 0.39	0,530886	0,768869	0,230966	0,471895	0,262784	0,334997
	SYP	1.02 ± 0.20	0.82 ± 0.31	1.09 ± 0.48	0.69 ± 0.29	0,131839	0,395517	0,674822	0,833604	🟩 0,008418	🟩 0,039284
	SYT1	1.01 ± 0.18	0.88 ± 0.42	1.15 ± 0.63	0.83 ± 0.48	0,357715	0,628649	0,509828	0,775885	0,238214	0,322742
	SYT13	1.04 ± 0.30	0.83 ± 0.38	1.07 ± 0.45	1.05 ± 0.54	0,246964	0,525382	0,868258	0,958836	0,981224	0,987973
	SYT16	1.03 ± 0.25	0.85 ± 0.36	1.05 ± 0.49	1.00 ± 0.59	0,250182	0,525382	0,895977	0,958836	0,868671	0,944451

🟩 downregulation

🟥 upregulation

Supplementary Table 1

	Gene	Gene name	Taqman reference
Housekeeping genes	*GUS-B*	β-glucuronidase	Hs00939627_m1
	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1	Hs00958026_m1
Hubs	*GSK3B*	*Glycogen synthase kinase 3 beta*	Hs01047719_m1
	LAPTM5	*Lysosomal protein transmembrane 5*	Hs00988563_m1
	PSMA3	*Proteasome (prosome, macropain) subunit, alpha type, 3*	Hs00541061_m1
	STIP1	*Stress-induced-phosphoprotein 1*	Hs00428979_m1
	SYK	*Spleen associated tyrosine kinase*	Hs00895377_m1
	TPI1	*Triosephosphate isomerase 1*	Hs03806547_s1
	YWHAB	*Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide*	Hs00793604_m1
	CYCS	*Cytochrome c, somatic*	Hs01588973_m1
	ATP6V1A	*ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A*	Hs01097169_m1
	AIF1	*Allograft inflammatory factor 1*	Hs00741549_g1
Axonema	*DNAAF1*	*Dynein axonemal assembly factor 1*	Hs00698399_m1
	DNAH11	*Dynein axonemal heavy chain 11*	Hs00361951_m1
	DNAH2	*Dynein axonemal heavy chain 2*	Hs00325838_m1
	DNAH5	*Dynein axonemal heavy chain 5*	Hs00292485_m1
	DNAH7	*Dynein axonemal heavy chain 7*	Hs00324265_m1
	DNAH9	*Dynein axonemal heavy chain 9*	Hs00242096_m1
	DNAI1	*Dynein axonemal intermediate chain 1*	Hs00201755_m1
Taste receptors	*TAS2R4*	*Taste 2 receptor member 4*	Hs00249946_s1
	TAS2R5	*Taste 2 receptor member 5*	Hs01549633_s1
	TAS2R14	*Taste 2 receptor member 14*	Hs00256800_s1
	TAS2R50	*Taste 2 receptor member 50*	Hs00604351_s1
	TAS2R10	*Taste 2 receptor member 10*	Hs00256794_s1
	TAS2R13	*Taste 2 receptor member 13*	Hs01059805_s1
RNA/DNA	*KAT2A*	*Lysine acetyltransferase 2A*	Hs00221499_m1
	PNPT1	*Polyribonucleotide nucleotidyltransferase 1*	Hs01105971_m1
	PAPOLA	*Poly(A) polymerase alpha*	Hs04276840_m1
	RELA	*RELA proto-oncogene, NF-kB subunit*	Hs00153294_m1
	DOT1L	*DOT1 like histone lysine methyltransferase*	Hs01588547_m1
Chaperones	*DNAJA1*	*DnaJ (Hsp40) homolog, subfamily A, member 1*	Hs00266011_m1
	DNAJA4	*DnaJ (Hsp40) homolog, subfamily A, member 4*	Hs00388055_m1
	DNAJB1	*DnaJ (Hsp40) homolog, subfamily B, member 1*	Hs00428680_m1
	DNAJB4	*DnaJ (Hsp40) homolog, subfamily B, member 4*	Hs00199826_m1
	HSPA1A	*Heat shock 70kDa protein 1A*	Hs00359147_s1
	HSPA4	*Heat shock 70kDa protein 4*	Hs00382884_m1
	HSPA5	*Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)*	Hs99999174_m1
	HSPA6	*Heat shock 70kDa protein 6 (HSP70B)*	Hs00275682_s1
	HSPD1	*Heat shock 60kDa protein 1 (chaperonin)*	Hs01036757_m1
	HSPE1	*MOB family member 4, phocein*	Hs00854653_s1
Neurotransmitters and synapses	*GABBR2*	*Gamma-aminobutyric acid (GABA) B receptor, 2*	Hs01554996_m1
	GABRA1	*Gamma-aminobutyric acid (GABA) A receptor, alpha 1*	Hs00971228_m1
	GAD1	*Glutamate decarboxylase 1 (brain, 67kDa)*	Hs01065893_m1
	GRIN2A	*Glutamate receptor, ionotropic, N-methyl D-aspartate 2A*	Hs00168219_m1
	GRIN2B	*Glutamate receptor, ionotropic, N-methyl D-aspartate 2B*	Hs01002012_m1
	NETO1	*neuropilin (NRP) and tolloid (TLL)-like 1*	Hs00371151_m1
	RAB3A	*RAB3A, member RAS oncogene family*	Hs00923221_m1
	RPH3A	*Rabphilin 3A homolog (mouse)*	Hs00934263_m1
	SNAP25	*Synaptosomal-associated protein, 25kDa*	Hs00938962_m1
	STXBP1	*Syntaxin binding protein 1*	Hs01119036_m1
	SYP	*Synaptophysin*	Hs00300531_m1
	SYT1	*Synaptotagmin I*	Hs00194572_m1
	SYT13	*Synaptotagmin XIII*	Hs00951871_m1
	SYT16	*Synaptotagmin XVI*	Hs00736645_m1

Supplementary Table 2: Number of DEGs for different thresholds for each comparison iLBD, PD, DLB and middle-aged individuals (MA)

	iLBDvsMA	PDvsMA	DLBvsMA	PDvsDLB	PDvsiLBD	iLBDvsDLB
upReg-B > 0	1	0	18	192	3	26
downReg-B > 0	13	0	76	42	0	55
upReg-Adjusted-p-val < 0.01	0	0	0	0	0	0
downReg-Adjusted-p-val < 0.01	0	0	0	0	0	0
upReg-Adjusted-p-val < 0.05	0	0	236	1691	0	1041
downReg-Adjusted-p-val < 0.05	0	0	881	673	0	609
upReg-Adjusted-p-val < 0.25	7	0	1124	2573	0	2478
downReg-Adjusted-p-val < 0.25	42	0	2156	1513	0	1600
upReg-P value < 0.01	38	16	244	1375	68	870
downReg-P value < 0.01	116	24	897	449	6	512
upReg-P value < 0.05	230	94	681	2097	168	1779
downReg-P value < 0.05	394	125	1680	999	21	1048

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0015988	8.08E-09	22.6620562	2.94730652	14	17
GO:0015991	8.08E-09	22.6620562	2.94730652	14	17
GO:0045333	1.10E-08	4.38518519	11.7892261	32	68
GO:1902600	1.20E-07	5.65991903	7.10820983	22	41
GO:0007005	6.87E-07	2.20590164	37.4481299	66	216
GO:0009161	1.08E-06	3.0787037	15.7767584	35	91
GO:0015992	1.32E-06	3.85739249	10.2288873	26	59
GO:0006091	1.33E-06	2.35801803	29.1263232	54	168
GO:0009123	1.54E-06	2.95634807	16.6436133	36	96
GO:0006818	1.95E-06	3.74286423	10.4022583	26	60
GO:0015980	2.21E-06	2.53169338	23.0583392	45	133
GO:0009141	2.49E-06	2.98648649	15.6033874	34	90
GO:0009167	2.49E-06	2.98648649	15.6033874	34	90
GO:0009126	3.33E-06	2.93324349	15.7767584	34	91
GO:0046034	4.69E-06	3.1300972	13.3495648	30	77
GO:0022904	5.25E-06	4.42753899	7.2815808	20	42
GO:0051648	6.01E-06	2.77593971	16.8169842	35	97
GO:1901564	6.33E-06	1.59230189	113.384615	154	654
GO:0022900	8.24E-06	4.23382451	7.45495178	20	43
GO:0009144	1.21E-05	2.8673633	14.5631616	31	84
GO:0009060	1.33E-05	6.16647806	4.33427429	14	25
GO:0009205	1.54E-05	2.88127132	14.0430487	30	81
GO:0046128	1.65E-05	2.52686508	18.8974359	37	109
GO:0006101	1.78E-05	8.85858586	2.94730652	11	17
GO:0051656	1.86E-05	2.37641988	21.8447424	41	126
GO:0009199	2.04E-05	2.82504624	14.2164197	30	82
GO:0006810	2.07E-05	1.41605763	247.227005	296	1426
GO:0009119	2.08E-05	2.49152642	19.0708069	37	110
GO:0051650	2.15E-05	2.65343238	16.2968713	33	94
GO:0042278	2.61E-05	2.45714286	19.2441778	37	111
GO:0006753	3.22E-05	1.93813184	38.3149847	62	221
GO:0044765	3.27E-05	1.41698869	217.927311	264	1257
GO:0072350	3.87E-05	7.59090909	3.12067749	11	18
GO:0002478	3.92E-05	3.34807692	9.36203246	22	54
GO:0042773	4.31E-05	6.44597701	3.6407904	12	21
GO:0042775	4.31E-05	6.44597701	3.6407904	12	21
GO:0019884	5.48E-05	3.24568765	9.53540343	22	55
GO:0006099	6.78E-05	8.04218249	2.77393554	10	16
GO:0009117	6.90E-05	1.89502206	37.6215008	60	217
GO:0015031	7.06E-05	1.55046501	94.1404375	127	543

GO:0006418	7.95E-05	12.8431642	1.90708069	8	11
GO:0055086	8.15E-05	1.85007813	40.2220654	63	232
GO:0022406	0.00010166	4.27366792	5.54787109	15	32
GO:0051234	0.00010198	1.36978448	252.601506	297	1457
GO:0019882	0.00011581	2.85129819	11.2691131	24	65
GO:0051640	0.00012098	2.05081888	26.5257586	45	153
GO:0061025	0.00013091	3.09382936	9.36203246	21	54
GO:0009116	0.00013995	2.21226481	20.6311456	37	119
GO:0009259	0.00014551	1.99532734	28.2594684	47	163
GO:0006107	0.00015488	Inf	0.86685486	5	5
GO:1902578	0.00016426	1.36546261	227.115973	269	1310
GO:0048002	0.00018792	2.89147609	10.2288873	22	59
GO:1901657	0.00019279	2.14141713	21.6713714	38	125
GO:0043648	0.00019548	3.69116967	6.41472595	16	37
GO:0044257	0.00019908	1.99363381	27.0458716	45	156
GO:0032400	0.00020221	9.62962963	2.08045166	8	12
GO:0051875	0.00020221	9.62962963	2.08045166	8	12
GO:0051603	0.00021027	2.04211126	24.7920489	42	143
GO:0006119	0.00021224	4.48895028	4.68101623	13	27
GO:0009150	0.00021643	1.96758321	27.9127264	46	161
GO:0019941	0.00023135	2.11646508	21.8447424	38	126
GO:0019637	0.00023996	1.61965047	60.853211	86	351
GO:0090382	0.00026507	6.02819807	3.12067749	10	18
GO:0019693	0.00027278	1.92654589	28.9529522	47	167
GO:0043632	0.0002767	2.09207375	22.0181134	38	127
GO:0006511	0.00029531	2.1069103	21.3246295	37	123
GO:0006879	0.00033413	4.18848987	4.8543872	13	28
GO:0048278	0.00033413	4.18848987	4.8543872	13	28
GO:0006163	0.00042645	1.87789561	29.4730652	47	170
GO:0043038	0.00044615	7.70150892	2.25382263	8	13
GO:0043039	0.00044615	7.70150892	2.25382263	8	13
GO:0033059	0.00047342	5.35686994	3.29404846	10	19
GO:0033572	0.00047342	5.35686994	3.29404846	10	19
GO:0010501	0.00054354	14.4131327	1.38696777	6	8
GO:0010498	0.00054639	2.12047697	18.8974359	33	109
GO:0051649	0.00059473	1.38881758	136.789697	169	789
GO:0051436	0.00060678	4.13793103	4.50764526	12	26
GO:0071702	0.00060721	1.38903978	135.922842	168	784
GO:0006904	0.00070699	4.42171717	3.98753235	11	23
GO:0043473	0.00071344	3.29765802	6.41472595	15	37
GO:0045184	0.00075127	1.4336768	100.901905	129	582
GO:0015682	0.00080127	4.81980743	3.46741943	10	20
GO:0072512	0.00080127	4.81980743	3.46741943	10	20

GO:0006105	0.00089738	Inf	0.69348389	4	4
GO:0006538	0.00089738	Inf	0.69348389	4	4
GO:0051439	0.00092241	3.86096552	4.68101623	12	27
GO:0006836	0.00092898	2.03817247	19.4175488	33	112
GO:0007611	0.00092898	2.03817247	19.4175488	33	112
GO:0043161	0.00094919	2.11856589	17.1637262	30	99
GO:0006732	0.0011006	2.01210938	19.5909198	33	113
GO:0051641	0.00119839	1.3429051	156.380616	188	902
GO:0006996	0.00120532	1.33388689	167.649729	200	967
GO:0034220	0.00121128	1.5011981	67.267937	90	388
GO:1903050	0.001252	2.24979193	13.6963068	25	79
GO:0006520	0.0012847	1.86903759	24.445307	39	141
GO:0072521	0.00132637	1.74371876	31.7268878	48	183
GO:0044281	0.0013534	1.35153292	141.817455	172	818
GO:0033238	0.00136062	3.02112188	6.76146789	15	39
GO:0000209	0.00150101	2.55656144	9.53540343	19	55
GO:0046364	0.00172763	3.07355715	6.24135498	14	36
GO:0019886	0.00196557	3.40478702	5.02775817	12	29
GO:0051352	0.00196557	3.40478702	5.02775817	12	29
GO:0051444	0.00196557	3.40478702	5.02775817	12	29
GO:0006977	0.00201039	4.01421366	3.81416137	10	22
GO:0051437	0.00201039	4.01421366	3.81416137	10	22
GO:0072413	0.00201039	4.01421366	3.81416137	10	22
GO:0072431	0.00201039	4.01421366	3.81416137	10	22
GO:1902400	0.00201039	4.01421366	3.81416137	10	22
GO:1902402	0.00201039	4.01421366	3.81416137	10	22
GO:1902403	0.00201039	4.01421366	3.81416137	10	22
GO:0008104	0.00201778	1.35313627	125.347212	153	723
GO:0006839	0.0022552	1.97255247	18.030581	30	104
GO:0016051	0.00225927	2.31303961	11.2691131	21	65
GO:0046907	0.00228964	1.3977157	92.7534698	117	535
GO:0046916	0.00234497	2.93908233	6.41472595	14	37
GO:0042364	0.00238694	11.9945355	1.2135968	5	7
GO:0044380	0.00238694	11.9945355	1.2135968	5	7
GO:0070979	0.00238694	11.9945355	1.2135968	5	7
GO:0023061	0.0024378	1.67895501	32.5937426	48	188
GO:0071158	0.00244363	3.53434343	4.50764526	11	26
GO:1903052	0.00246467	2.48845619	9.18866149	18	53
GO:0010822	0.00249138	2.56918403	8.49517761	17	49
GO:0055085	0.0025017	1.40412903	87.5523406	111	505
GO:0017157	0.00252002	2.18731806	12.8294519	23	74
GO:0006887	0.00257038	1.73920254	27.7393554	42	160
GO:0055082	0.00266545	1.63406326	36.0611621	52	208

GO:0006120	0.00273326	4.80932785	2.77393554	8	16
GO:0007214	0.00273326	4.80932785	2.77393554	8	16
GO:0016050	0.00287608	2.11694505	13.6963068	24	79
GO:0032401	0.00297091	7.20246238	1.73370972	6	10
GO:0032402	0.00297091	7.20246238	1.73370972	6	10
GO:0051904	0.00297091	7.20246238	1.73370972	6	10
GO:0051905	0.00297091	7.20246238	1.73370972	6	10
GO:0031145	0.00301301	3.70436991	3.98753235	10	23
GO:0072395	0.00301301	3.70436991	3.98753235	10	23
GO:0072401	0.00301301	3.70436991	3.98753235	10	23
GO:0072422	0.00301301	3.70436991	3.98753235	10	23
GO:1903362	0.00301539	2.03602377	15.2566455	26	88
GO:0098660	0.00303825	1.53738839	47.3302752	65	273
GO:0050890	0.00318703	1.81396618	22.3648553	35	129
GO:0016079	0.00321319	2.57716135	7.97506469	16	46
GO:1903321	0.00321319	2.57716135	7.97506469	16	46
GO:0007268	0.00329384	1.44213716	67.6146789	88	390
GO:0032543	0.00348946	3.3125	4.68101623	11	27
GO:0016192	0.00352118	1.41653666	74.8962597	96	432
GO:1903364	0.00375088	2.29825905	10.2288873	19	59
GO:0051046	0.00381574	1.57658932	39.1818396	55	226
GO:0006094	0.0038193	3.0446461	5.37450012	12	31
GO:0019319	0.0038193	3.0446461	5.37450012	12	31
GO:0051443	0.0038193	3.0446461	5.37450012	12	31
GO:0072698	0.00386739	19.1705321	0.86685486	4	5
GO:0033036	0.00393762	1.30833942	141.297342	168	815
GO:0006873	0.00393888	1.66605143	29.9931781	44	173
GO:0010970	0.00402381	2.85007534	6.067984	13	35
GO:0030705	0.00412617	2.70240664	6.76146789	14	39
GO:0007093	0.00414777	2.5865651	7.45495178	15	43
GO:0031397	0.00414777	2.5865651	7.45495178	15	43
GO:2000060	0.00437694	3.43878955	4.16090332	10	24
GO:1903530	0.00447824	1.58963622	36.0611621	51	208
GO:0051186	0.00457133	1.77907279	22.0181134	34	127
GO:0007269	0.00459932	1.92713339	16.4702423	27	95
GO:0006006	0.00471756	2.0892911	12.6560809	22	73
GO:0044710	0.004934	1.24476398	262.830393	294	1516
GO:0034622	0.00510247	1.55521488	38.8350976	54	224
GO:0002495	0.00516779	2.89158621	5.54787109	12	32
GO:0002504	0.00516779	2.89158621	5.54787109	12	32
GO:0051351	0.00516779	2.89158621	5.54787109	12	32
GO:0006106	0.00519357	Inf	0.52011291	3	3
GO:0006122	0.00519357	Inf	0.52011291	3	3

GO:0071539	0.00519357	Inf	0.52011291	3	3
GO:0085020	0.00519357	Inf	0.52011291	3	3
GO:0030163	0.00530481	1.59568733	33.8073394	48	195
GO:0002220	0.00530985	2.4966568	7.62832275	15	44
GO:0002223	0.00530985	2.4966568	7.62832275	15	44
GO:0006399	0.00532165	2.72537833	6.24135498	13	36
GO:0055072	0.00532165	2.72537833	6.24135498	13	36
GO:0048489	0.00533995	2.15031768	11.2691131	20	65
GO:0097480	0.00533995	2.15031768	11.2691131	20	65
GO:0008637	0.00535969	2.59772316	6.93483886	14	40
GO:0051340	0.00535969	2.59772316	6.93483886	14	40
GO:0051438	0.00535969	2.59772316	6.93483886	14	40
GO:0006086	0.00545927	7.99408015	1.38696777	5	8
GO:0006891	0.00545927	7.99408015	1.38696777	5	8
GO:0010447	0.00545927	7.99408015	1.38696777	5	8
GO:0010510	0.00545927	7.99408015	1.38696777	5	8
GO:0006085	0.00558511	5.76032832	1.90708069	6	11
GO:0006513	0.00558511	5.76032832	1.90708069	6	11
GO:0034453	0.00558511	5.76032832	1.90708069	6	11
GO:1902582	0.00569466	1.37321123	81.4843566	102	470
GO:0050877	0.00588953	1.4418311	57.3857916	75	331
GO:0007267	0.0059994	1.35361603	89.8061633	111	518
GO:0002479	0.00618389	3.2086199	4.33427429	10	25
GO:0031571	0.00618389	3.2086199	4.33427429	10	25
GO:0044783	0.00618389	3.2086199	4.33427429	10	25
GO:0044819	0.00618389	3.2086199	4.33427429	10	25
GO:0010821	0.00644995	2.10296525	11.4424841	20	66
GO:0097479	0.00644995	2.10296525	11.4424841	20	66
GO:0044265	0.00665017	1.55619837	35.8877911	50	207
GO:0006734	0.00671861	3.84526749	3.12067749	8	18
GO:0008286	0.0068025	1.77135477	20.1110327	31	116
GO:0038061	0.00686952	2.75310345	5.72124206	12	33
GO:0045921	0.00686952	2.75310345	5.72124206	12	33
GO:0032940	0.00688831	1.42977587	57.7325335	75	333
GO:0042787	0.00693402	2.61107274	6.41472595	13	37
GO:0007270	0.0073758	1.95368323	13.8696777	23	80
GO:0042176	0.00739875	1.72429435	21.8447424	33	126
GO:0030003	0.00741033	1.6116694	29.2996942	42	169
GO:0046903	0.00745371	1.40231128	64.1472595	82	370
GO:0070585	0.00774163	2.05762782	11.6158551	20	67
GO:0044708	0.00783039	1.56928744	32.7671136	46	189
GO:1901135	0.00801355	1.39702581	64.3206304	82	371
GO:0009268	0.00813569	4.20239726	2.60056457	7	15

GO:0098662	0.00821225	1.49134162	42.3025171	57	244
GO:0009108	0.0084194	2.3342418	7.97506469	15	46
GO:0055076	0.0084194	2.3342418	7.97506469	15	46
GO:0006521	0.00852156	3.00722146	4.50764526	10	26
GO:0032482	0.00852156	3.00722146	4.50764526	10	26
GO:0042590	0.00852156	3.00722146	4.50764526	10	26
GO:2000058	0.00852156	3.00722146	4.50764526	10	26
GO:0090068	0.0088273	2.12062824	10.2288873	18	59
GO:0071156	0.00898338	2.62721003	5.89461303	12	34
GO:0001963	0.00955151	4.79890561	2.08045166	6	12
GO:0006536	0.00955151	4.79890561	2.08045166	6	12
GO:0007018	0.00991971	2.03995667	11.0957422	19	64
GO:0072655	0.00991971	2.03995667	11.0957422	19	64

Term	Genes	padjust
energy couple	ATP6V1F ATP	1.95E-05
ATP hydrolysi	ATP6V1F ATP	1.95E-05
cellular respir	COX8A NDUF	1.95E-05
hydrogen ion	COX8A ATP6\	0.00015998
mitochondrio	TOMM20 VPS	0.00073293
ribonucleosid	COX8A NDUF	0.00088503
proton transp	COX8A ATP6\	0.00088503
generation of	COX8A NDUF	0.00088503
nucleoside m	DGUOK COX8	0.00091468
hydrogen tran	COX8A ATP6\	0.00102102
energy deriva	COX8A NDUF	0.00102102
nucleoside tri	DGUOK ENTP	0.00102102
purine ribonu	COX8A NDUF	0.00102102
purine nucleo	COX8A NDUF	0.00126841
ATP metaboli	COX8A NDUF	0.00166881
respiratory el	COX8A NDUF	0.00175031
vesicle localiz	VPS33B CDK5	0.00187656
organonitrog	DGUOK BECN	0.00187656
electron trans	COX8A NDUF	0.00231388
purine nucleo	DGUOK COX8	0.00323162
aerobic respi	IDH3G OXA1L	0.00338231
purine ribonu	COX8A NDUF	0.00374138
purine ribonu	DGUOK COX8	0.00381861
citrate metab	IDH3G MDH2	0.0039556
establishmen	BECN1 CDK5	0.0039556
ribonucleosid	COX8A NDUF	0.0039556
transport	TOMM20 VPS	0.0039556
ribonucleosid	DGUOK COX8	0.0039556
establishmen	CDK5 SEC23A	0.0039556
purine nucleo	DGUOK COX8	0.00464664
nucleoside ph	DGUOK ENTP	0.00544191
single-organis	TOMM20 VPS	0.00544191
tricarboxylic a	IDH3G MDH2	0.00614669
antigen proce	SEC23A PSMI	0.00614669
ATP synthesis	COX8A NDUF	0.00638998
mitochondria	COX8A NDUF	0.00638998
antigen proce	SEC23A PSMI	0.00790375
tricarboxylic a	IDH3G MDH2	0.00940813
nucleotide m	DGUOK COX8	0.00940813
protein trans	TOMM20 VPS	0.00940813

tRNA aminoa	SARS YARS FA	0.01033599
nucleobase-c	DGUOK ENTP	0.01035322
membrane do	VPS33B RAB3	0.01236079
establishmen	TOMM20 VPS	0.01236079
antigen proce	SEC23A RAB3	0.01372479
organelle loca	VPS33B BECN	0.01402605
membrane fu	VPS11 VPS33	0.0148544
nucleoside m	DGUOK COX8	0.0155493
ribonucleotid	COX8A NDUF	0.01583695
oxaloacetate	GOT1 MDH2	0.01651965
single-organis	TOMM20 VPS	0.01717592
antigen proce	SEC23A PSMD	0.01891925
glycosyl comp	DGUOK COX8	0.01891925
dicarboxylic a	IDH3G GAD1	0.01891925
cellular prote	VPS11 ERLEC1	0.01891925
melanosome	VPS33B DCTN	0.01891925
pigment gran	VPS33B DCTN	0.01891925
proteolysis in	ERLEC1 USP5	0.01918422
oxidative pho	COX8A NDUF	0.01918422
purine ribonu	COX8A NDUF	0.01923672
modification-	ERLEC1 USP5	0.02022612
organophosp	DGUOK ENTP	0.02064021
phagosome m	ATP6V1F ATP	0.02243834
ribose phospl	COX8A NDUF	0.02270192
modification-	ERLEC1 USP5	0.02270192
ubiquitin-dep	ERLEC1 USP5	0.023862
cellular iron i	ATP6V1F ATP	0.0262048
vesicle dockir	VPS33B RAB3	0.0262048
purine nucleo	DGUOK COX8	0.03296054
amino acid ac	SARS YARS FA	0.03351129
tRNA aminoa	SARS YARS FA	0.03351129
cellular pigme	VPS33B DCTN	0.03458526
transferrin tra	ATP6V1F ATP	0.03458526
RNA seconda	DHX36 DDX25	0.03885209
proteasomal	ERLEC1 USP5	0.03885209
establishmen	TOMM20 VPS	0.04151597
negative regu	PSMD8 PSMC	0.04151597
organic subst	TOMM20 VPS	0.04151597
vesicle dockir	VPS33B RAB3	0.04755969
pigmentation	VPS33B C12o	0.04755969
establishmen	TOMM20 VPS	0.04946299
ferric iron tra	ATP6V1F ATP	0.051484
trivalent inor	ATP6V1F ATP	0.051484

succinate me	GAD1 GAD2	0.05629813
glutamate ca	GAD1 GAD2	0.05629813
regulation of	PSMD8 PSM	0.05629813
neurotransmi	SLC32A1 CDK	0.05629813
learning or m	RCAN2 CDK5	0.05629813
proteasome-	ERLEC1 USP5	0.05687649
coenzyme m	IDH3G PNPO	0.06521637
cellular locali	TOMM20 VP	0.06945994
organelle org	TOMM20 SSS	0.06945994
ion transmem	COX8A MPC2	0.06945994
regulation of	USP5 PSMD8	0.07103113
cellular amin	GAD1 GAD2	0.07211881
purine-contai	DGUOK COX8	0.07368276
small molecu	DGUOK ENTP	0.0740427
regulation of	PSMD8 PSM	0.0740427
protein polyu	PSMD8 PSM	0.08085765
monosacchar	AKR1A1 GOT	0.09213473
antigen proce	SEC23A ACTR	0.09694422
negative regu	PSMD8 PSM	0.09694422
negative regu	PSMD8 PSM	0.09694422
DNA damage	PSMD8 PSM	0.09694422
positive regul	PSMD8 PSM	0.09694422
signal transd	PSMD8 PSM	0.09694422
signal transd	PSMD8 PSM	0.09694422
intracellular s	PSMD8 PSM	0.09694422
signal transd	PSMD8 PSM	0.09694422
signal transd	PSMD8 PSM	0.09694422
protein locali	TOMM20 VP	0.09694422
mitochondria	TOMM20 VP	0.10662565
carbohydrate	MAS1 AKR1A	0.10662565
intracellular t	TOMM20 VP	0.10711083
cellular trans	ATP6V1F ATP	0.10787745
water-soluble	AKR1A1 PNP	0.10787745
protein locali	HTR2A DCTN	0.10787745
protein K11-li	UBE2E2 PARK	0.10787745
signal release	SLC32A1 SNX	0.10838131
positive regul	PSMD8 PSM	0.10838131
positive regul	USP5 PSMD8	0.10838131
positive regul	VPS11 BECN1	0.10838131
transmembra	TOMM20 CO	0.10838131
regulation of	SNX4 CDK5 N	0.10838131
exocytosis	VPS33B TUB	0.10966267
cellular chem	ATP6V1F ATP	0.11281633

mitochondria	NDUFB5 NDU	0.11387863
gamma-amin	GABRA3 CACI	0.11387863
vesicle organi	VPS11 VPS33	0.11652937
establishmen	DCTN2 RAB27	0.11652937
melanosome	DCTN2 RAB27	0.11652937
pigment gran	DCTN2 RAB27	0.11652937
establishmen	DCTN2 RAB27	0.11652937
anaphase-prc	PSMD8 PSMC	0.11652937
signal transdu	PSMD8 PSMC	0.11652937
signal transdu	PSMD8 PSMC	0.11652937
signal transdu	PSMD8 PSMC	0.11652937
regulation of	VPS11 USP5 F	0.11652937
inorganic ion	COX8A ATP6V	0.11656828
cognition	RCAN2 CDK5	0.1206755
synaptic vesic	CDK5 NAPA R	0.1206755
negative regu	CDK5 PSMD8	0.1206755
synaptic trans	SLC32A1 CDK	0.12283947
mitochondria	MRPL15 MRP	0.12923135
vesicle-media	VPS11 VPS33	0.12950654
positive regul	VPS11 USP5 F	0.13578872
regulation of	SNX4 CDK5 N	0.13578872
gluconeogene	GOT1 MDH2	0.13578872
hexose biosyr	GOT1 MDH2	0.13578872
positive regul	PSMD8 PSMC	0.13578872
protein locali	DCTN2 SNX10	0.13658785
macromolecu	TOMM20 VPS	0.13729431
cellular ion hc	ATP6V1F ATP	0.13729431
microtubule-l	COPG1 NDEL1	0.13934412
cytoskeleton-	COPG1 NDEL1	0.14089223
mitotic cell cy	ZWILCH PSMI	0.14089223
negative regu	CDK5 PSMD8	0.14089223
positive regul	PSMD8 PSMC	0.14773545
regulation of	SNX4 CDK5 N	0.15020395
cofactor meta	IDH3G PNPO	0.15234876
neurotransmi	SLC32A1 CDK	0.15234876
glucose meta	AKR1A1 GOT1	0.15530082
single-organis	DGUOK ENTP	0.1573746
cellular macro	SNRPB TUBA4	0.1573746
antigen proce	SEC23A ACTR	0.1573746
antigen proce	SEC23A ACTR	0.1573746
positive regul	PSMD8 PSMC	0.1573746
fumarate met	GOT1 FH GOT	0.1573746
mitochondria	CYCS UQCRC1	0.1573746

protein locali	DCTN2 SNX1	0.1573746
protein K6-lin	PARK2 UBE2T	0.1573746
protein catab	VPS11 ERLEC	0.1573746
innate immu	PAK1 PSMD8	0.1573746
stimulatory C	PAK1 PSMD8	0.1573746
tRNA metabo	SARS YARS F	0.1573746
iron ion hom	ATP6V1F ATP	0.1573746
synaptic vesi	CDK5 NAPA R	0.1573746
establishmen	CDK5 NAPA R	0.1573746
apoptotic mit	SLC25A4 YW	0.1573746
regulation of	PSMD8 PSM	0.1573746
regulation of	PSMD8 PSM	0.1573746
acetyl-CoA bi	PDHB DLD DL	0.1573746
intra-Golgi ve	NAPA COG1	0.1573746
response to a	ASIC2 CHP1 L	0.1573746
regulation of	PDHB DLD DL	0.1573746
acetyl-CoA bi	PDHB ACLY D	0.15843292
protein mon	PARK2 FBXL2	0.15843292
microtubule	BECN1 SEH1L	0.15843292
single-organi	TOMM20 VP	0.16068575
neurological	DFNA5 RCAN	0.1653097
cell-cell signa	SLC32A1 SNX	0.167512
antigen proce	PSMD8 PSM	0.16912155
mitotic G1 D	PSMD8 PSM	0.16912155
G1 DNA dam	PSMD8 PSM	0.16912155
mitotic G1/S	PSMD8 PSM	0.16912155
regulation of	VPS11 BECN1	0.17460706
synaptic vesi	CDK5 NAPA R	0.17460706
cellular macr	VPS11 ERLEC	0.17911801
NADH metab	IDH3G MDH2	0.18005189
insulin recept	ATP6V1F ATP	0.18096228
NIK/NF-kapp	MAS1 PSMD	0.18096228
positive regul	SNX4 CDK5 P	0.18096228
secretion by	VPS33B CBLN	0.18096228
protein ubiqu	PSMD8 PSM	0.18127032
neuron-neur	CDK5 NAPA R	0.1909145
regulation of	VPS11 ERLEC	0.1909145
cellular catio	ATP6V1F ATP	0.1909145
secretion	VPS33B CBLN	0.19110885
protein locali	TOMM20 VP	0.19754111
single-organi	RCAN2 CDK5	0.19885474
carbohydrate	DGUOK COX8	0.2025414
response to p	ASIC2 CHP1 L	0.2046587

inorganic cati	COX8A ATP6V	0.20561475
coenzyme bic	PNPO PDHB A	0.20751355
transition me	ATP6V1F ATP	0.20751355
regulation of	PSMD8 PSMC	0.20751355
Rab protein s	DNAJC27 RAB	0.20751355
antigen proce	PSMD8 PSMC	0.20751355
regulation of	PSMD8 PSMC	0.20751355
positive regul	BECN1 PLCB1	0.21398172
regulation of	CDK5 PSMD8	0.21677989
synaptic trans	CDK5 RAB3B	0.22842254
glutamate me	GAD1 GAD2	0.22842254
microtubule-l	COPG1 SPA17	0.23511918
establishmen	TOMM20 VPS	0.23511918

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0045926	1.67E-06	6.67616048	2.24864738	12	79
GO:0010043	2.14E-06	15.7883772	0.65466949	7	23
GO:0019219	5.52E-06	2.44962515	24.8489767	46	873
GO:0060255	1.05E-05	2.25090791	38.3123971	61	1346
GO:0051252	1.10E-05	2.43551146	22.2587626	42	782
GO:0071294	1.16E-05	25.387931	0.34156669	5	12
GO:0006357	1.46E-05	2.823148	12.1256175	28	426
GO:0090304	2.54E-05	2.23360364	29.6024465	50	1040
GO:1903507	3.40E-05	3.11298851	8.02681722	21	282
GO:0045934	3.42E-05	2.95374597	9.30769231	23	327
GO:0010558	3.59E-05	2.94329207	9.3361562	23	328
GO:0050793	3.65E-05	2.38431677	19.3839097	37	681
GO:0051171	3.85E-05	2.21917184	27.4961186	47	966
GO:0010468	3.90E-05	2.24149235	25.8452129	45	908
GO:1902679	3.99E-05	3.07522727	8.11220889	21	285
GO:0001701	4.11E-05	4.67600193	3.04563632	12	107
GO:0009890	4.31E-05	2.83975457	10.1046813	24	355
GO:0051253	4.66E-05	3.03831461	8.19760056	21	288
GO:0000122	4.85E-05	3.61608212	5.20889203	16	183
GO:1990267	4.97E-05	7.23893805	1.36626676	8	48
GO:0016070	5.15E-05	2.19806141	26.9553046	46	947
GO:0010556	5.64E-05	2.22529706	24.5643378	43	863
GO:0006366	6.30E-05	2.57061263	13.1218537	28	461
GO:0006355	6.44E-05	2.27161863	21.4617737	39	754
GO:0040007	6.71E-05	2.87837838	9.05151729	22	318
GO:0006351	7.03E-05	2.24376502	22.3441543	40	785
GO:2000112	7.04E-05	2.21297468	23.9665961	42	842
GO:0071276	7.05E-05	28.2051282	0.25617502	4	9
GO:0019222	7.16E-05	2.05590232	47.1077394	68	1655
GO:1903506	7.49E-05	2.25254065	21.6040932	39	759
GO:0097659	8.15E-05	2.2255144	22.4864738	40	790
GO:2001141	8.20E-05	2.24122052	21.6894848	39	762
GO:0019438	9.26E-05	2.14323561	26.7275935	45	939
GO:0010605	0.00010023	2.365117	16.423665	32	577
GO:0018130	0.00010032	2.13408731	26.8129852	45	942
GO:0051172	0.00010421	2.7204455	9.99082569	23	351
GO:0080090	0.00011066	2.02803933	39.2232416	59	1378
GO:0031323	0.00011252	2.02327359	40.16255	60	1411
GO:0034654	0.00011919	2.12571429	26.1583157	44	919
GO:0006725	0.00012354	2.02891958	36.6330275	56	1287

GO:0009059	0.00014578	2.04738364	31.5095272	50	1107
GO:0032774	0.00014873	2.15144673	23.0842155	40	811
GO:0043170	0.00017809	2.00292013	60.2865208	80	2118
GO:0009889	0.00018157	2.07728074	26.6137379	44	935
GO:0045892	0.00018952	2.86655773	7.71371442	19	271
GO:0010467	0.0001908	2.01186573	32.7050106	51	1149
GO:1901360	0.00024373	1.95634191	38.3977888	57	1349
GO:1901362	0.00025358	2.0288966	27.8376853	45	978
GO:0031327	0.00025465	2.59304703	9.90543402	22	348
GO:0044260	0.00027351	1.93992346	55.81769	75	1961
GO:0031326	0.00027753	2.03892827	26.2437074	43	922
GO:0034645	0.00028039	1.99184764	30.5417549	48	1073
GO:0030278	0.00028438	5.4459843	1.73629734	8	61
GO:0042475	0.00030712	10.428499	0.6262056	5	22
GO:0031324	0.0003096	2.22334537	16.6513761	31	585
GO:0040008	0.00031039	3.02607023	6.09127264	16	214
GO:0009790	0.00031773	2.82004593	7.37214773	18	259
GO:0051726	0.00031773	2.82004593	7.37214773	18	259
GO:0006139	0.00032653	1.94391361	35.1529052	53	1235
GO:0042476	0.00032873	7.64347826	0.96777229	6	34
GO:0044271	0.00034617	1.96878726	30.7979299	48	1082
GO:2000113	0.00035559	2.64163916	8.76687838	20	308
GO:0010629	0.00037159	2.56980769	9.47847565	21	333
GO:0046483	0.00047491	1.90025482	36.5476359	54	1284
GO:0065007	0.0004793	2.18932662	84.8793225	101	2982
GO:0051254	0.00050002	2.45351474	10.3893202	22	365
GO:0045944	0.00053026	2.77173913	7.03058104	17	247
GO:0050789	0.00053666	2.07937599	80.3820278	97	2824
GO:0045913	0.00057862	8.85775862	0.71159727	5	25
GO:0043009	0.0006032	3.2160701	4.61115032	13	162
GO:0045935	0.00061064	2.32652107	11.983298	24	421
GO:0048519	0.00061888	1.88182454	35.0959774	52	1233
GO:0009792	0.00063984	3.19382716	4.63961421	13	163
GO:0045893	0.00067279	2.44229358	9.90543402	21	348
GO:1903508	0.00067279	2.44229358	9.90543402	21	348
GO:0010628	0.00070088	2.30084582	12.0971536	24	425
GO:0051093	0.0007317	2.68504544	7.22982828	17	254
GO:1902680	0.00078249	2.41024169	10.0192896	21	352
GO:1901576	0.0009379	1.81674609	41.1872501	58	1447
GO:0001655	0.00101841	3.63063063	3.13102799	10	110
GO:0031958	0.00113483	20.9745763	0.22771113	3	8
GO:2000810	0.00113483	20.9745763	0.22771113	3	8
GO:0044249	0.00117461	1.79621302	40.5895084	57	1426

GO:0009892	0.00125368	1.99750312	18.8430957	32	662
GO:0046620	0.00138496	7.07758621	0.85391673	5	30
GO:0042733	0.00140265	10.0512821	0.51235004	4	18
GO:0001503	0.00143575	3.45345345	3.27334745	10	115
GO:0051173	0.00148247	2.16261428	12.7518231	24	448
GO:0010557	0.00150348	2.23172906	11.2717008	22	396
GO:0048856	0.00155205	1.76118742	43.8343919	60	1540
GO:0009058	0.00164696	1.75887334	42.0411668	58	1477
GO:0046621	0.00166701	17.4745763	0.25617502	3	9
GO:0008283	0.00181534	2.04336831	15.2566455	27	536
GO:0001822	0.00182459	3.60714286	2.81792519	9	99
GO:0006807	0.00187705	1.74028234	45.0868031	61	1584
GO:0031328	0.00192858	2.1468435	12.2394731	23	430
GO:0034641	0.00193831	1.74198568	42.2973418	58	1486
GO:0010675	0.00194065	5.20339343	1.33780287	6	47
GO:0010564	0.00202241	3.07692308	4.01340861	11	141
GO:0051148	0.00212513	8.79059829	0.56927782	4	20
GO:0061005	0.00212513	8.79059829	0.56927782	4	20
GO:0009891	0.00231556	2.1122449	12.4102564	23	436
GO:0051154	0.0023322	14.9745763	0.28463891	3	10
GO:0035509	0.00236604	69.394958	0.08539167	2	3
GO:0044332	0.00236604	69.394958	0.08539167	2	3
GO:1903347	0.00236604	69.394958	0.08539167	2	3
GO:0045595	0.00238766	2.04756795	13.9757704	25	491
GO:0006109	0.002413	4.95894843	1.39473065	6	49
GO:0003007	0.00246169	4.23684211	1.8786168	7	66
GO:0048869	0.00246248	1.74664172	34.3559163	49	1207
GO:0006473	0.00246942	6.09542212	0.96777229	5	34
GO:0030856	0.00246942	6.09542212	0.96777229	5	34
GO:0009888	0.00252577	2.03770477	14.0326982	25	493
GO:0046686	0.00256803	8.27149321	0.59774171	4	21
GO:0072001	0.00257047	3.41306391	2.96024465	9	104
GO:0007507	0.00296941	2.91459854	4.21265585	11	148
GO:0010676	0.00307046	7.81006648	0.6262056	4	22
GO:0071704	0.00313218	1.76968601	74.3761468	89	2613
GO:2000677	0.00314055	13.0995763	0.3131028	3	11
GO:0045596	0.00315361	2.62620217	5.52199482	13	194
GO:0044767	0.00315889	1.68559643	46.9084921	62	1648
GO:0030326	0.00319734	5.69938821	1.02470007	5	36
GO:0035113	0.00319734	5.69938821	1.02470007	5	36
GO:0033043	0.00324154	2.30039304	8.28299224	17	291
GO:0048598	0.00329746	2.87122302	4.26958363	11	150
GO:0007049	0.003387	2.0406247	12.780287	23	449

GO:0008152	0.00347288	1.88440398	85.6763115	99	3010
GO:0030279	0.00363612	7.39721098	0.65466949	4	23
GO:0048871	0.00376245	3.49492769	2.56175018	8	90
GO:0044237	0.00377997	1.74042951	73.6360856	88	2587
GO:0045786	0.00378643	2.98488571	3.7287697	10	131
GO:0072358	0.00386849	2.25623794	8.42531169	17	296
GO:0072359	0.00386849	2.25623794	8.42531169	17	296
GO:0009653	0.00398923	1.77262194	24.4504822	37	859
GO:0044262	0.00402871	3.45196716	2.59021407	8	91
GO:2000756	0.00410105	11.6412429	0.34156669	3	12
GO:0048523	0.00423236	1.69996956	32.4772995	46	1141
GO:0007009	0.00424866	3.14173024	3.18795578	9	112
GO:0030522	0.00437123	3.78096757	2.07786403	7	73
GO:0014706	0.00450775	3.11074863	3.21641967	9	113
GO:0048729	0.00452777	2.6125364	5.09503646	12	179
GO:0060429	0.00459297	2.21363759	8.56763115	17	301
GO:0032502	0.00459334	1.64648008	47.5631616	62	1671
GO:0010604	0.00460009	1.79715989	21.2340626	33	746
GO:0006378	0.00464393	34.6890756	0.11385556	2	4
GO:0010586	0.00464393	34.6890756	0.11385556	2	4
GO:0035507	0.00464393	34.6890756	0.11385556	2	4
GO:0035947	0.00464393	34.6890756	0.11385556	2	4
GO:0043153	0.00464393	34.6890756	0.11385556	2	4
GO:0043631	0.00464393	34.6890756	0.11385556	2	4
GO:0048368	0.00464393	34.6890756	0.11385556	2	4
GO:2000628	0.00464393	34.6890756	0.11385556	2	4
GO:2000630	0.00464393	34.6890756	0.11385556	2	4
GO:0007517	0.00477904	3.08035714	3.24488356	9	114
GO:0009887	0.00478439	2.32445665	7.17290049	15	252
GO:0010035	0.00491347	2.70952381	4.49729475	11	158
GO:0045667	0.00509769	5.04310345	1.13855563	5	40
GO:0060537	0.00566991	2.99255952	3.33027523	9	117
GO:0010942	0.00572423	2.42901235	5.9204893	13	208
GO:0009893	0.00579694	1.69919023	27.6099741	40	970
GO:0022402	0.00598194	2.10204894	9.53540343	18	335
GO:2000026	0.00600555	1.8863315	14.9720066	25	526
GO:0048513	0.00636315	1.7200692	24.251235	36	852
GO:0035872	0.00650892	9.52003082	0.39849447	3	14
GO:0045668	0.00650892	9.52003082	0.39849447	3	14
GO:0051153	0.00660165	6.10479376	0.76852505	4	27
GO:0051146	0.00675901	3.46076998	2.24864738	7	79
GO:0048518	0.00683827	1.6099061	43.4928252	57	1528
GO:0044238	0.00696648	1.65180613	71.5866855	85	2515

GO:0061061	0.00697366	2.4587156	5.37967537	12	189
GO:0016569	0.00723618	3.41252103	2.27711127	7	80
GO:0016570	0.00723618	3.41252103	2.27711127	7	80
GO:0048738	0.00726328	3.86561265	1.73629734	6	61
GO:0009648	0.007596	23.1204482	0.14231945	2	5
GO:0009950	0.007596	23.1204482	0.14231945	2	5
GO:0030903	0.007596	23.1204482	0.14231945	2	5
GO:0034629	0.007596	23.1204482	0.14231945	2	5
GO:0043616	0.007596	23.1204482	0.14231945	2	5
GO:0048339	0.007596	23.1204482	0.14231945	2	5
GO:0072364	0.007596	23.1204482	0.14231945	2	5
GO:0090527	0.007596	23.1204482	0.14231945	2	5
GO:2000696	0.007596	23.1204482	0.14231945	2	5
GO:0043543	0.00768701	4.5214412	1.2524112	5	44
GO:0051493	0.00774306	2.66599933	4.12726417	10	145
GO:0003012	0.00783361	2.83082707	3.50105857	9	123
GO:0015931	0.00845515	4.40732759	1.28087509	5	45
GO:0035107	0.00845515	4.40732759	1.28087509	5	45
GO:0035108	0.00845515	4.40732759	1.28087509	5	45
GO:0071241	0.00848824	3.72814645	1.79322512	6	63
GO:0043065	0.00853797	2.38814397	5.52199482	12	194
GO:0043068	0.0092359	2.36098923	5.57892261	12	196
GO:0035265	0.00927497	4.29878049	1.30933898	5	46
GO:0003229	0.00960681	8.05149935	0.45542225	3	16
GO:0035850	0.00960681	8.05149935	0.45542225	3	16
GO:0045599	0.00960681	8.05149935	0.45542225	3	16
GO:1901983	0.00960681	8.05149935	0.45542225	3	16
GO:0045778	0.00965469	5.3964497	0.85391673	4	30
GO:0018205	0.0098552	3.6	1.85015291	6	65
GO:0051239	0.00998322	1.69715833	21.4617737	32	754

Term
negative regulation of growth
response to zinc ion
regulation of nucleobase-containing compound metabolic process
regulation of macromolecule metabolic process
regulation of RNA metabolic process
cellular response to zinc ion
regulation of transcription from RNA polymerase II promoter
nucleic acid metabolic process
negative regulation of nucleic acid-templated transcription
negative regulation of nucleobase-containing compound metabolic process
negative regulation of macromolecule biosynthetic process
regulation of developmental process
regulation of nitrogen compound metabolic process
regulation of gene expression
negative regulation of RNA biosynthetic process
in utero embryonic development
negative regulation of biosynthetic process
negative regulation of RNA metabolic process
negative regulation of transcription from RNA polymerase II promoter
response to transition metal nanoparticle
RNA metabolic process
regulation of macromolecule biosynthetic process
transcription from RNA polymerase II promoter
regulation of transcription, DNA-templated
growth
transcription, DNA-templated
regulation of cellular macromolecule biosynthetic process
cellular response to cadmium ion
regulation of metabolic process
regulation of nucleic acid-templated transcription
nucleic acid-templated transcription
regulation of RNA biosynthetic process
aromatic compound biosynthetic process
negative regulation of macromolecule metabolic process
heterocycle biosynthetic process
negative regulation of nitrogen compound metabolic process
regulation of primary metabolic process
regulation of cellular metabolic process
nucleobase-containing compound biosynthetic process
cellular aromatic compound metabolic process

macromolecule biosynthetic process
RNA biosynthetic process
macromolecule metabolic process
regulation of biosynthetic process
negative regulation of transcription, DNA-templated
gene expression
organic cyclic compound metabolic process
organic cyclic compound biosynthetic process
negative regulation of cellular biosynthetic process
cellular macromolecule metabolic process
regulation of cellular biosynthetic process
cellular macromolecule biosynthetic process
regulation of ossification
odontogenesis of dentin-containing tooth
negative regulation of cellular metabolic process
regulation of growth
embryo development
regulation of cell cycle
nucleobase-containing compound metabolic process
odontogenesis
cellular nitrogen compound biosynthetic process
negative regulation of cellular macromolecule biosynthetic process
negative regulation of gene expression
heterocycle metabolic process
biological regulation
positive regulation of RNA metabolic process
positive regulation of transcription from RNA polymerase II promoter
regulation of biological process
positive regulation of carbohydrate metabolic process
chordate embryonic development
positive regulation of nucleobase-containing compound metabolic process
negative regulation of biological process
embryo development ending in birth or egg hatching
positive regulation of transcription, DNA-templated
positive regulation of nucleic acid-templated transcription
positive regulation of gene expression
negative regulation of developmental process
positive regulation of RNA biosynthetic process
organic substance biosynthetic process
urogenital system development
corticosteroid receptor signaling pathway
regulation of bicellular tight junction assembly
cellular biosynthetic process

negative regulation of metabolic process
regulation of organ growth
embryonic digit morphogenesis
ossification
positive regulation of nitrogen compound metabolic process
positive regulation of macromolecule biosynthetic process
anatomical structure development
biosynthetic process
negative regulation of organ growth
cell proliferation
kidney development
nitrogen compound metabolic process
positive regulation of cellular biosynthetic process
cellular nitrogen compound metabolic process
regulation of cellular carbohydrate metabolic process
regulation of cell cycle process
negative regulation of muscle cell differentiation
cell differentiation involved in kidney development
positive regulation of biosynthetic process
negative regulation of striated muscle cell differentiation
negative regulation of myosin-light-chain-phosphatase activity
Wnt signaling pathway involved in dorsal/ventral axis specification
negative regulation of bicellular tight junction assembly
regulation of cell differentiation
regulation of carbohydrate metabolic process
heart morphogenesis
cellular developmental process
protein acetylation
regulation of epithelial cell differentiation
tissue development
response to cadmium ion
renal system development
heart development
positive regulation of cellular carbohydrate metabolic process
organic substance metabolic process
regulation of transcription regulatory region DNA binding
negative regulation of cell differentiation
single-organism developmental process
embryonic limb morphogenesis
embryonic appendage morphogenesis
regulation of organelle organization
embryonic morphogenesis
cell cycle

metabolic process
negative regulation of ossification
multicellular organismal homeostasis
cellular metabolic process
negative regulation of cell cycle
cardiovascular system development
circulatory system development
anatomical structure morphogenesis
cellular carbohydrate metabolic process
regulation of peptidyl-lysine acetylation
negative regulation of cellular process
plasma membrane organization
intracellular receptor signaling pathway
striated muscle tissue development
tissue morphogenesis
epithelium development
developmental process
positive regulation of macromolecule metabolic process
mRNA polyadenylation
miRNA metabolic process
regulation of myosin-light-chain-phosphatase activity
regulation of gluconeogenesis by regulation of transcription from RNA polymerase II promoter
entrainment of circadian clock by photoperiod
RNA polyadenylation
lateral mesoderm development
regulation of miRNA metabolic process
positive regulation of miRNA metabolic process
muscle organ development
organ morphogenesis
response to inorganic substance
regulation of osteoblast differentiation
muscle tissue development
positive regulation of cell death
positive regulation of metabolic process
cell cycle process
regulation of multicellular organismal development
organ development
nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway
negative regulation of osteoblast differentiation
regulation of striated muscle cell differentiation
striated muscle cell differentiation
positive regulation of biological process
primary metabolic process

muscle structure development
covalent chromatin modification
histone modification
cardiac muscle tissue development
photoperiodism
dorsal/ventral axis specification
notochord development
cellular protein complex localization
keratinocyte proliferation
paraxial mesoderm development
regulation of cellular ketone metabolic process by regulation of transcription from RNA polymerase II pro
actin filament reorganization
regulation of epithelial cell differentiation involved in kidney development
protein acylation
regulation of cytoskeleton organization
muscle system process
nucleobase-containing compound transport
appendage morphogenesis
limb morphogenesis
cellular response to inorganic substance
positive regulation of apoptotic process
positive regulation of programmed cell death
organ growth
ventricular cardiac muscle tissue development
epithelial cell differentiation involved in kidney development
negative regulation of fat cell differentiation
regulation of protein acetylation
positive regulation of ossification
peptidyl-lysine modification
regulation of multicellular organismal process

Genes	padjust
PNPT1 GJA1	0.00327742
P2RX7 MT1F	0.00327742
KLF15 PNPT1	0.00564802
KLF15 PNPT1	0.00593641
KLF15 PNPT1	0.00593641
MT1F MT1G	0.00593641
KLF15 WWC3	0.00638488
KLF15 PNPT1	0.00751821
WWC3 HDAC	0.00751821
GJA1 WWC3	0.00751821
GJA1 WWC3	0.00751821
PNPT1 PRKX	0.00751821
KLF15 PNPT1	0.00751821
KLF15 ZNF47	0.00751821
WWC3 HDAC	0.00751821
GJA1 CAPN2	0.00751821
GJA1 WWC3	0.00751821
WWC3 HDAC	0.00751821
WWC3 HDAC	0.00751821
P2RX7 MT1F	0.00751821
KLF15 PNPT1	0.00751821
KLF15 ZNF47	0.00757111
KLF15 WWC3	0.00757111
KLF15 ZNF47	0.00757111
IL17RB PNPT	0.00757111
KLF15 ZNF47	0.00757111
KLF15 ZNF47	0.00757111
MT1F MT1G	0.00757111
KLF15 PNPT1	0.00757111
KLF15 ZNF47	0.00765942
KLF15 ZNF47	0.00785739
KLF15 ZNF47	0.00785739
KLF15 ZNF47	0.00860181
KLF15 GJA1	0.00879129
KLF15 ZNF47	0.00879129
GJA1 WWC3	0.00887805
KLF15 PNPT1	0.00908154
KLF15 PNPT1	0.00908154
KLF15 ZNF47	0.00937321
KLF15 PNPT1	0.00947281

PRELP KLF15	0.01086101
KLF15 ZNF47	0.01086101
PRELP KLF15	0.01265593
KLF15 ZNF47	0.01265593
WWC3 HDAC	0.01272128
KLF15 PNPT1	0.01272128
KLF15 PNPT1	0.01590472
KLF15 ZNF47	0.01593908
GJA1 WWC3	0.01593908
KLF15 PNPT1	0.01645627
KLF15 ZNF47	0.01645627
KLF15 ZNF47	0.01645627
LRP4 GJA1 P2	0.01645627
LRP4 MSX1 A	0.01680145
KLF15 GJA1	0.01680145
IL17RB PNPT	0.01680145
LRP4 GJA1 EY	0.01680145
PNPT1 NUPR	0.01680145
KLF15 PNPT1	0.0168037
LRP4 MSX1 A	0.0168037
KLF15 ZNF47	0.01740482
GJA1 WWC3	0.01759009
GJA1 WWC3	0.01809017
KLF15 PNPT1	0.02261567
IL17RB KLF15	0.02261567
KLF15 PNPT1	0.02323565
KLF15 RBM1	0.02420513
IL17RB KLF15	0.02420513
P2RX7 RAMP	0.02571911
GJA1 CAPN2	0.02636263
KLF15 PNPT1	0.02636263
KLF15 PNPT1	0.02636263
GJA1 CAPN2	0.02688209
KLF15 RBM1	0.02751277
KLF15 RBM1	0.02751277
KLF15 GJA1 P	0.02828409
LRP4 GJA1 W	0.0291445
KLF15 RBM1	0.03076803
PRELP KLF15	0.03641177
KLF15 PRKX L	0.03904322
RBM14 CRY1	0.04244557
GJA1 IKBKB R	0.04244557
PRELP KLF15	0.04340386

KLF15 GJA1 W	0.04577408
GJA1 WWC3	0.04997275
LRP4 GJA1 M	0.05002232
LRP4 GJA1 P2	0.05061418
KLF15 PNPT1	0.05166755
KLF15 RBM14	0.05181083
PRELP KLF15	0.05289053
PRELP KLF15	0.05550806
GJA1 WWC3	0.05557301
AKR1C2 PRKX	0.05953214
KLF15 PRKX L	0.05953214
PRELP KLF15	0.06059919
KLF15 RBM14	0.06073444
KLF15 PNPT1	0.06073444
P2RX7 HDAC4	0.06073444
RBM14 KLHL2	0.06265384
HDAC4 MSX1	0.0645324
KLF15 PRKX P	0.0645324
KLF15 RBM14	0.06762232
HDAC4 MSX1	0.06762232
IKBKB ROCK1	0.06762232
LRP4 LRP2	0.06762232
IKBKB ROCK1	0.06762232
PRKX LRP4 GJ	0.06762232
P2RX7 HDAC4	0.06762232
GJA1 MSX1 R	0.06762232
KLF15 PNPT1	0.06762232
KLF15 NUPR1	0.06762232
PRKX IKBKB P	0.06762232
KLF15 AKR1C	0.06855322
MT1F MT1G	0.06855322
KLF15 PRKX L	0.06855322
GJA1 MSX1 R	0.07851026
P2RX7 KAT2A	0.07972556
PRELP KLF15	0.07972556
MSX1 KAT2A	0.07972556
LRP4 TOB2 H	0.07972556
PRELP KLF15	0.07972556
LRP4 GJA1 M	0.07972556
LRP4 GJA1 M	0.07972556
PAN2 P2RX7	0.08017573
LRP4 GJA1 EY	0.08090637
PNPT1 NUPR1	0.08244399

PRELP KLF15	0.08386874
LRP4 HDAC4	0.08712477
P2RX7 ADGR	0.08864872
PRELP KLF15	0.08864872
PNPT1 NUPR	0.08864872
PRKX GJA1 M	0.08920803
PRKX GJA1 M	0.08920803
PNPT1 PRKX	0.09130566
SLC5A3 P2RX	0.09152631
KLF15 FLCN K	0.09248466
KLF15 PNPT1	0.09309098
P2RX7 MTSS1	0.09309098
P2RX7 RBM1	0.09309098
GJA1 NUPR1	0.09309098
PRKX GJA1 E	0.09309098
KLF15 AKR1C	0.09309098
PRELP KLF15	0.09309098
KLF15 PNPT1	0.09309098
PNPT1 PAPOL	0.09309098
PNPT1 RELA	0.09309098
IKBKB ROCK1	0.09309098
KAT2A FOXO	0.09309098
CRY1 RBM4B	0.09309098
PNPT1 PAPOL	0.09309098
ZIC2 YAP1	0.09309098
PNPT1 RELA	0.09309098
PNPT1 RELA	0.09309098
GJA1 NUPR1	0.09466925
PRKX LRP4 GJ	0.09466925
P2RX7 MT1F	0.09660006
GJA1 HDAC4	0.09958349
GJA1 NUPR1	0.11006084
NUPR1 P2RX	0.11041653
KLF15 PNPT1	0.11112002
PNPT1 RBM1	0.11369765
PRKX LRP4 GJ	0.11369765
KLF15 PRKX L	0.1197287
P2RX7 IKBKB	0.120987
HDAC4 PTCH	0.120987
HDAC4 MSX1	0.12197143
HDAC4 CAPN	0.12413102
KLF15 PNPT1	0.1248392
PRELP KLF15	0.125813

GJA1 NUPR1	0.125813
EYA2 RBM14	0.12800517
EYA2 RBM14	0.12800517
GJA1 RXRA PI	0.12800517
CRY1 RBM4B	0.12800517
LRP4 LRP2	0.12800517
YAP1 ID3	0.12800517
KLHL21 NACC	0.12800517
PTCH1 YAP1	0.12800517
YAP1 FOXC1	0.12800517
KAT2A FOXO	0.12800517
FRYL ARAP1	0.12800517
PRKX YAP1	0.12800517
KLF15 NUPR1	0.12883096
P2RX7 RBM1	0.12906501
KLF15 GJA1 C	0.12986847
PNPT1 GJA1	0.13774306
LRP4 GJA1 M	0.13774306
LRP4 GJA1 M	0.13774306
MT1F MT1G	0.13774306
NUPR1 P2RX	0.13782085
NUPR1 P2RX	0.14815804
GJA1 WWC3	0.14815804
RXRA PPP1R1	0.15030937
KLF15 PRKX Y	0.15030937
ID4 GPER1 FC	0.15030937
KLF15 FLCN K	0.15030937
GJA1 P2RX7 T	0.15030937
KLF15 HDAC4	0.15265609
PRKX LRP4 GJ	0.15386198

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0006955	1.65E-12	6.57976519	7.19266055	30	392
GO:0050865	2.94E-11	11.8419717	1.9266055	16	105
GO:0045321	7.86E-11	8.63694915	3.10091743	19	169
GO:0002694	9.11E-11	12.0282187	1.76146789	15	96
GO:0002684	1.03E-10	7.16194865	4.3853211	22	239
GO:0050867	1.34E-10	14.9745455	1.24770642	13	68
GO:0050670	7.50E-10	21.769958	0.69724771	10	38
GO:0032944	9.94E-10	21.0141988	0.71559633	10	39
GO:0002696	1.13E-09	14.1337907	1.19266055	12	65
GO:0046649	1.42E-09	8.79154242	2.47706422	16	135
GO:0046651	1.58E-09	16.1481876	0.97247706	11	53
GO:0042110	1.63E-09	10.5205882	1.81651376	14	99
GO:0070489	1.63E-09	10.5205882	1.81651376	14	99
GO:0071593	1.63E-09	10.5205882	1.81651376	14	99
GO:0032943	1.96E-09	15.7688303	0.99082569	11	54
GO:0002376	2.18E-09	4.38661818	12.0917431	34	659
GO:0002460	2.20E-09	19.0303309	0.7706422	10	42
GO:0070663	2.20E-09	19.0303309	0.7706422	10	42
GO:0001775	3.00E-09	6.11858761	4.73394495	21	258
GO:0070486	3.18E-09	9.92395833	1.90825688	14	104
GO:0070661	4.40E-09	14.4128295	1.06422018	11	58
GO:0050778	9.05E-09	7.08186346	3.21100917	17	175
GO:0007159	9.64E-09	9.00189394	2.0733945	14	113
GO:0051249	1.57E-08	10.8142292	1.48623853	12	81
GO:0006952	5.24E-08	4.35232558	8.36697248	26	456
GO:0002252	5.45E-08	6.18224044	3.6146789	17	197
GO:0034109	6.01E-08	7.65059267	2.3853211	14	130
GO:0002250	6.17E-08	12.6378676	1.06422018	10	58
GO:0051251	6.17E-08	12.6378676	1.06422018	10	58
GO:0050776	1.03E-07	5.30075881	4.73394495	19	258
GO:0016064	1.03E-07	25.6153169	0.42201835	7	23
GO:0002682	1.03E-07	4.4107039	7.44954128	24	406
GO:0050863	1.40E-07	11.4317425	1.1559633	10	63
GO:0042098	1.41E-07	17.5492063	0.64220183	8	35
GO:0019724	1.44E-07	24.1027341	0.44036697	7	24
GO:1903037	2.22E-07	10.8114496	1.21100917	10	66
GO:0042129	3.53E-07	20.4725352	0.49541284	7	27
GO:0002253	3.69E-07	6.4933364	2.75229358	14	150
GO:0034110	3.93E-07	10.0808824	1.28440367	10	70
GO:0002449	4.28E-07	14.7892857	0.73394495	8	40

GO:0002507	5.18E-07	225.513514	0.09174312	4	5
GO:0050870	1.11E-06	12.7752896	0.82568807	8	45
GO:0002443	1.18E-06	10.3369565	1.11926606	9	61
GO:0006959	1.24E-06	16.3583099	0.58715596	7	32
GO:0006950	1.40E-06	3.07519531	19.5045872	39	1063
GO:0045087	1.56E-06	4.53359073	5.08256881	18	277
GO:1903039	1.58E-06	12.1142857	0.86238532	8	47
GO:0034112	1.86E-06	11.8085714	0.88073394	8	48
GO:0032945	2.10E-06	35.6592466	0.23853211	5	13
GO:0050672	2.10E-06	35.6592466	0.23853211	5	13
GO:0045785	2.65E-06	7.04760408	1.94495413	11	106
GO:0006954	3.45E-06	5.67746479	2.8440367	13	155
GO:0002263	3.50E-06	10.7246753	0.95412844	8	52
GO:0002366	3.50E-06	10.7246753	0.95412844	8	52
GO:0030155	3.89E-06	5.21484375	3.33944954	14	182
GO:0070664	4.76E-06	28.5136986	0.27522936	5	15
GO:0022407	5.16E-06	7.33680057	1.68807339	10	92
GO:0002714	5.95E-06	Inf	0.05504587	3	3
GO:0002891	5.95E-06	Inf	0.05504587	3	3
GO:0002712	6.95E-06	56.3378378	0.14678899	4	8
GO:0002889	6.95E-06	56.3378378	0.14678899	4	8
GO:0050900	8.36E-06	6.90669371	1.77981651	10	97
GO:0002695	8.59E-06	15.7234848	0.51376147	6	28
GO:0007584	1.06E-05	9.05714286	1.10091743	8	60
GO:0022409	1.20E-05	8.88409704	1.11926606	8	61
GO:0002455	1.23E-05	45.0594595	0.16513761	4	9
GO:0016337	1.24E-05	4.66276738	3.68807339	14	201
GO:0048584	1.27E-05	3.17348008	10.3669725	25	565
GO:0002285	1.61E-05	13.8266667	0.56880734	6	31
GO:0002822	1.74E-05	20.3473581	0.34862385	5	19
GO:0002821	2.03E-05	37.5405405	0.18348624	4	10
GO:0002824	2.03E-05	37.5405405	0.18348624	4	10
GO:0002683	2.17E-05	6.93845285	1.57798165	9	86
GO:0050866	2.35E-05	12.7962963	0.60550459	6	33
GO:0002274	2.47E-05	9.6971831	0.89908257	7	49
GO:0002699	2.81E-05	12.3363095	0.62385321	6	34
GO:0002819	2.96E-05	17.7953767	0.3853211	5	21
GO:0098602	3.48E-05	4.21253034	4.03669725	14	220
GO:0050671	3.77E-05	16.7445608	0.40366972	5	22
GO:0098609	3.87E-05	3.95418927	4.62385321	15	252
GO:0006956	4.65E-05	28.1418919	0.22018349	4	12
GO:0032946	4.75E-05	15.8105023	0.42201835	5	23
GO:0002521	5.11E-05	5.48300054	2.18348624	10	119

GO:0009605	5.17E-05	2.7547234	13.4495413	28	733
GO:0051250	5.91E-05	14.9747657	0.44036697	5	24
GO:0034341	6.33E-05	10.4545455	0.71559633	6	39
GO:0002286	6.62E-05	25.009009	0.23853211	4	13
GO:0060443	6.62E-05	25.009009	0.23853211	4	13
GO:0070665	7.29E-05	14.2226027	0.4587156	5	25
GO:0042102	9.13E-05	22.5027027	0.25688073	4	14
GO:0007565	0.00011165	9.31531532	0.78899083	6	43
GO:0002705	0.00012283	20.4520885	0.27522936	4	15
GO:0031294	0.00012283	20.4520885	0.27522936	4	15
GO:0031295	0.00012283	20.4520885	0.27522936	4	15
GO:0072376	0.00012283	20.4520885	0.27522936	4	15
GO:1902105	0.00012935	7.24823944	1.1559633	7	63
GO:0019221	0.0001316	4.84218077	2.44036697	10	133
GO:0002703	0.00015378	11.8407534	0.53211009	5	29
GO:0048518	0.00015909	2.3449342	28.0366972	44	1528
GO:0040011	0.00016364	2.73746507	10.5688073	23	576
GO:0002757	0.00017905	4.6472886	2.53211009	10	138
GO:0002888	0.00019732	41.69	0.12844037	3	7
GO:0010575	0.00019732	41.69	0.12844037	3	7
GO:0002706	0.00020827	17.2972973	0.31192661	4	17
GO:0030595	0.00020894	8.19642857	0.88073394	6	48
GO:0034097	0.00024772	3.83261183	3.68807339	12	201
GO:0007155	0.00024855	2.88523927	8.03669725	19	438
GO:0022610	0.00024855	2.88523927	8.03669725	19	438
GO:0002495	0.00024978	10.5175038	0.58715596	5	32
GO:0002504	0.00024978	10.5175038	0.58715596	5	32
GO:0050896	0.00025207	2.40860632	41.6146789	57	2268
GO:0048583	0.00025335	2.36090327	18.7522936	33	1022
GO:0002520	0.00027176	3.79057592	3.72477064	12	203
GO:0009991	0.0002845	3.76988636	3.74311927	12	204
GO:0032845	0.00029352	7.64444444	0.93577982	6	51
GO:0001817	0.00029824	4.77320799	2.20183486	9	120
GO:0051704	0.00030403	2.70642105	9.55963303	21	521
GO:0001773	0.00031154	33.344	0.14678899	3	8
GO:0006958	0.00031154	33.344	0.14678899	3	8
GO:0010574	0.00031154	33.344	0.14678899	3	8
GO:0071345	0.00032546	3.96304621	3.24770642	11	177
GO:0044706	0.00032701	7.47644928	0.95412844	6	52
GO:0001794	0.00033243	Inf	0.03669725	2	2
GO:0001796	0.00033243	Inf	0.03669725	2	2
GO:0001798	0.00033243	Inf	0.03669725	2	2
GO:0002445	0.00033243	Inf	0.03669725	2	2

GO:0002524	0.00033243	Inf	0.03669725	2	2
GO:0002883	0.00033243	Inf	0.03669725	2	2
GO:0002885	0.00033243	Inf	0.03669725	2	2
GO:0002892	0.00033243	Inf	0.03669725	2	2
GO:0002894	0.00033243	Inf	0.03669725	2	2
GO:0007182	0.00033243	Inf	0.03669725	2	2
GO:0033211	0.00033243	Inf	0.03669725	2	2
GO:0071346	0.00033538	9.78743505	0.62385321	5	34
GO:0032844	0.00033772	4.68641785	2.23853211	9	122
GO:0016477	0.00034818	2.96077446	6.89908257	17	376
GO:0050864	0.00040659	14.0439189	0.36697248	4	20
GO:0050878	0.00042406	3.59294437	3.90825688	12	213
GO:0050852	0.00044155	9.15156871	0.66055046	5	36
GO:0002708	0.00046115	27.78	0.16513761	3	9
GO:0030593	0.00049531	13.2146264	0.3853211	4	21
GO:0032941	0.00049531	13.2146264	0.3853211	4	21
GO:0034103	0.00049531	13.2146264	0.3853211	4	21
GO:1990266	0.00049531	13.2146264	0.3853211	4	21
GO:0006928	0.00060912	2.46147615	11.5412844	23	629
GO:0009611	0.00062292	2.98778602	5.9266055	15	323
GO:0002920	0.00065009	23.8057143	0.18348624	3	10
GO:0010573	0.00065009	23.8057143	0.18348624	3	10
GO:0042130	0.00065009	23.8057143	0.18348624	3	10
GO:0048002	0.00065366	6.47798742	1.08256881	6	59
GO:0031667	0.00065394	3.62101097	3.52293578	11	192
GO:0001819	0.00067229	5.38704225	1.50458716	7	82
GO:0007589	0.00071268	11.8179232	0.42201835	4	23
GO:0008284	0.00072548	3.36363636	4.14678899	12	226
GO:0048870	0.0007394	2.74987193	7.35779817	17	401
GO:0051674	0.0007394	2.74987193	7.35779817	17	401
GO:0002573	0.00078243	6.23939394	1.11926606	6	61
GO:1904018	0.0008171	7.87100457	0.75229358	5	41
GO:0032101	0.00084841	3.29858215	4.22018349	12	230
GO:0007568	0.000896	5.10928864	1.57798165	7	86
GO:1903706	0.000896	5.10928864	1.57798165	7	86
GO:0001816	0.00097757	3.993083	2.58715596	9	141
GO:0002291	0.00098541	109.789474	0.05504587	2	3
GO:0002438	0.00098541	109.789474	0.05504587	2	3
GO:0002513	0.00098541	109.789474	0.05504587	2	3
GO:0002861	0.00098541	109.789474	0.05504587	2	3
GO:0002863	0.00098541	109.789474	0.05504587	2	3
GO:0002864	0.00098541	109.789474	0.05504587	2	3
GO:0002866	0.00098541	109.789474	0.05504587	2	3

GO:0019372	0.00098541	109.789474	0.05504587	2	3
GO:0030853	0.00098541	109.789474	0.05504587	2	3
GO:0035635	0.00098541	109.789474	0.05504587	2	3
GO:2000535	0.00098541	109.789474	0.05504587	2	3
GO:2001300	0.00098541	109.789474	0.05504587	2	3
GO:0060333	0.00099015	10.6872587	0.4587156	4	25
GO:0071621	0.00099015	10.6872587	0.4587156	4	25
GO:0097530	0.00099015	10.6872587	0.4587156	4	25
GO:0040012	0.00102625	3.22054627	4.31192661	12	235
GO:0019882	0.0010982	5.81073446	1.19266055	6	65
GO:0030098	0.0010982	5.81073446	1.19266055	6	65
GO:0050730	0.0010982	5.81073446	1.19266055	6	65
GO:0050851	0.00113439	7.26027397	0.80733945	5	44
GO:0002886	0.00116065	18.5066667	0.22018349	3	12
GO:0007566	0.00116065	18.5066667	0.22018349	3	12
GO:0050871	0.00116065	18.5066667	0.22018349	3	12
GO:1901658	0.00116065	18.5066667	0.22018349	3	12
GO:0042127	0.00118478	2.62147909	7.66972477	17	418
GO:0032879	0.00120828	2.23460026	14.4770642	26	789
GO:0051716	0.00121758	2.07284805	35.2844037	49	1923
GO:0097529	0.00125808	7.07705479	0.82568807	5	45
GO:0070372	0.00128885	5.61748634	1.2293578	6	67
GO:0022612	0.00139148	6.90277314	0.8440367	5	46
GO:0051239	0.00143066	2.22843388	13.8348624	25	754
GO:0002702	0.001489	16.652	0.23853211	3	13
GO:0097028	0.001489	16.652	0.23853211	3	13
GO:0070887	0.00149212	2.19573643	14.6788991	26	800
GO:0032103	0.00150389	5.43650794	1.26605505	6	69
GO:0051701	0.00153505	6.73679061	0.86238532	5	47
GO:0030879	0.00153715	9.34459459	0.51376147	4	28
GO:0031100	0.00153715	9.34459459	0.51376147	4	28
GO:0051240	0.00170798	2.52364211	7.9266055	17	432
GO:0070371	0.0017453	5.26666667	1.30275229	6	71
GO:0019886	0.00175849	8.96864865	0.53211009	4	29
GO:0002697	0.00182297	4.47276995	1.77981651	7	97
GO:1903034	0.00182297	4.47276995	1.77981651	7	97
GO:0048771	0.00185455	6.42745953	0.89908257	5	49
GO:0002532	0.00187018	15.1345455	0.25688073	3	14
GO:0002283	0.00194735	54.8815789	0.0733945	2	4
GO:0006957	0.00194735	54.8815789	0.0733945	2	4
GO:0016139	0.00194735	54.8815789	0.0733945	2	4
GO:0042754	0.00194735	54.8815789	0.0733945	2	4
GO:0070254	0.00194735	54.8815789	0.0733945	2	4

GO:0045619	0.00200104	8.62162162	0.55045872	4	30
GO:0060326	0.00201513	5.10696517	1.33944954	6	73
GO:0030097	0.00205607	3.3005618	3.44954128	10	188
GO:0007166	0.00223908	2.12123116	15.0825688	26	822
GO:0042592	0.00224645	2.45128146	8.12844037	17	443
GO:0002429	0.00230176	4.27824393	1.85321101	7	101
GO:0030099	0.00230176	4.27824393	1.85321101	7	101
GO:0031529	0.00230701	13.87	0.27522936	3	15
GO:0045124	0.00230701	13.87	0.27522936	3	15
GO:0001676	0.00255383	8.0019305	0.58715596	4	32
GO:0002764	0.00269503	3.17011129	3.57798165	10	195
GO:0048534	0.00269503	3.17011129	3.57798165	10	195
GO:0030334	0.0027981	3.15227704	3.59633028	10	196
GO:0050764	0.00280213	12.8	0.29357798	3	16
GO:0050868	0.00280213	12.8	0.29357798	3	16
GO:0002478	0.002864	5.76460721	0.99082569	5	54
GO:0051384	0.002864	5.76460721	0.99082569	5	54
GO:0046849	0.00286605	7.72413793	0.60550459	4	33
GO:0048660	0.00286605	7.72413793	0.60550459	4	33
GO:0008283	0.0029921	2.2772842	9.83486239	19	536
GO:0031347	0.00301376	3.11717772	3.63302752	10	198
GO:0019884	0.00310583	5.64794521	1.00917431	5	55
GO:0033559	0.00320348	7.46486486	0.62385321	4	34
GO:0002639	0.00320698	36.5789474	0.09174312	2	5
GO:0002675	0.00320698	36.5789474	0.09174312	2	5
GO:0016137	0.00320698	36.5789474	0.09174312	2	5
GO:0044058	0.00320698	36.5789474	0.09174312	2	5
GO:0045577	0.00320698	36.5789474	0.09174312	2	5
GO:0032570	0.00335796	11.8828571	0.31192661	3	17
GO:0071482	0.00335796	11.8828571	0.31192661	3	17
GO:1903038	0.00335796	11.8828571	0.31192661	3	17
GO:0042060	0.00348079	2.88079602	4.33027523	11	236
GO:0048659	0.00356706	7.22231909	0.64220183	4	35
GO:0031960	0.0039198	5.32437322	1.06422018	5	58
GO:0031349	0.00392607	3.85739437	2.03669725	7	111
GO:0002761	0.00395775	6.99493243	0.66055046	4	36
GO:0015696	0.00395775	6.99493243	0.66055046	4	36
GO:1902107	0.00395775	6.99493243	0.66055046	4	36
GO:0007186	0.00396192	2.82760868	4.40366972	11	240
GO:0019369	0.00397674	11.088	0.33027523	3	18
GO:0046456	0.00397674	11.088	0.33027523	3	18
GO:1901570	0.00397674	11.088	0.33027523	3	18
GO:0072659	0.00410277	4.375	1.5412844	6	84

GO:0006631	0.00412697	3.81971831	2.05504587	7	112
GO:0015672	0.00422178	2.80170576	4.44036697	11	242
GO:0048872	0.00422222	5.22450533	1.08256881	5	59
GO:0048732	0.0043356	3.78275312	2.0733945	7	113
GO:1990778	0.00435094	4.3185654	1.55963303	6	85
GO:1903036	0.00437647	6.78132678	0.67889908	4	37
GO:2000145	0.00460416	2.92132353	3.85321101	10	210
GO:0033993	0.00463707	2.76368159	4.49541284	11	245
GO:0046850	0.00466053	10.3925	0.34862385	3	19
GO:0001821	0.00475334	27.4276316	0.11009174	2	6
GO:0030852	0.00475334	27.4276316	0.11009174	2	6
GO:0033008	0.00475334	27.4276316	0.11009174	2	6
GO:0042119	0.00475334	27.4276316	0.11009174	2	6
GO:0042554	0.00475334	27.4276316	0.11009174	2	6
GO:0043306	0.00475334	27.4276316	0.11009174	2	6
GO:0050832	0.00475334	27.4276316	0.11009174	2	6
GO:0051608	0.00475334	27.4276316	0.11009174	2	6
GO:0072678	0.00475334	27.4276316	0.11009174	2	6
GO:0090312	0.00475334	27.4276316	0.11009174	2	6
GO:0044255	0.00477414	2.52745098	5.85321101	13	319
GO:0052547	0.00488041	4.20987654	1.59633028	6	87
GO:0051270	0.00493164	2.73886921	4.53211009	11	247
GO:0045766	0.00530164	6.39073359	0.71559633	4	39
GO:0030260	0.00541123	9.77882353	0.36697248	3	20
GO:0034111	0.00541123	9.77882353	0.36697248	3	20
GO:0044409	0.00541123	9.77882353	0.36697248	3	20
GO:0045621	0.00541123	9.77882353	0.36697248	3	20
GO:0051806	0.00541123	9.77882353	0.36697248	3	20
GO:0051828	0.00541123	9.77882353	0.36697248	3	20
GO:0052126	0.00541123	9.77882353	0.36697248	3	20
GO:0052192	0.00541123	9.77882353	0.36697248	3	20
GO:0030336	0.00560009	4.85947095	1.1559633	5	63
GO:0042221	0.00617935	1.86201877	21.412844	32	1167
GO:0001776	0.00623055	9.23333333	0.3853211	3	21
GO:0002700	0.00623055	9.23333333	0.3853211	3	21
GO:0050729	0.00623055	9.23333333	0.3853211	3	21
GO:0007596	0.00625459	2.96220356	3.39449541	9	185
GO:0070374	0.0063496	6.04236669	0.75229358	4	41
GO:1903708	0.0063496	6.04236669	0.75229358	4	41
GO:0051048	0.00639653	4.69520548	1.19266055	5	65
GO:0009620	0.00657576	21.9368421	0.12844037	2	7
GO:0033005	0.00657576	21.9368421	0.12844037	2	7
GO:0036230	0.00657576	21.9368421	0.12844037	2	7

GO:0043011	0.00657576	21.9368421	0.12844037	2	7
GO:0043302	0.00657576	21.9368421	0.12844037	2	7
GO:0050856	0.00657576	21.9368421	0.12844037	2	7
GO:0007599	0.00670365	2.92745481	3.43119266	9	187
GO:0050817	0.00670365	2.92745481	3.43119266	9	187
GO:0006636	0.00712006	8.74526316	0.40366972	3	22
GO:0030183	0.00712006	8.74526316	0.40366972	3	22
GO:0050777	0.00712006	8.74526316	0.40366972	3	22
GO:2000146	0.00726956	4.54153778	1.2293578	5	67
GO:0010033	0.0073729	1.92003485	15.559633	25	848
GO:0030217	0.00752704	5.72972973	0.78899083	4	43
GO:0051046	0.00768662	2.69403595	4.14678899	10	226
GO:0002275	0.00808116	8.306	0.42201835	3	23
GO:0019915	0.00808116	8.306	0.42201835	3	23
GO:0045453	0.00808116	8.306	0.42201835	3	23
GO:0045670	0.00808116	8.306	0.42201835	3	23
GO:0010951	0.00816631	5.58513514	0.80733945	4	44
GO:0006915	0.00863	2.06654064	10.0366972	18	547
GO:0002437	0.00866383	18.2763158	0.14678899	2	8
GO:0002637	0.00866383	18.2763158	0.14678899	2	8
GO:0019370	0.00866383	18.2763158	0.14678899	2	8
GO:0050850	0.00866383	18.2763158	0.14678899	2	8
GO:0018108	0.00867801	3.69655797	1.79816514	6	98
GO:0018212	0.00910552	3.65591398	1.81651376	6	99
GO:0002444	0.00911513	7.90857143	0.44036697	3	24
GO:1903076	0.00911513	7.90857143	0.44036697	3	24
GO:1904375	0.00911513	7.90857143	0.44036697	3	24
GO:0044403	0.00933427	2.76480111	3.6146789	9	197
GO:0044419	0.00933427	2.76480111	3.6146789	9	197
GO:0012501	0.00946666	2.04438202	10.1284404	18	552
GO:0010466	0.00954969	5.31660232	0.8440367	4	46
GO:0042113	0.00954969	5.31660232	0.8440367	4	46

Term	Genes	padjust
immune resp	CSF1R APBB1	4.86E-09
regulation of	HLA-DPB1 AIF	4.32E-08
leukocyte act	APBB1IP HLA-	6.04E-08
regulation of	HLA-DPB1 AIF	6.04E-08
positive regul	CSF1R HLA-D	6.04E-08
positive regul	HLA-DPB1 AIF	6.58E-08
regulation of	HLA-DPB1 AIF	3.15E-07
regulation of	HLA-DPB1 AIF	3.43E-07
positive regul	HLA-DPB1 AIF	3.43E-07
lymphocyte a	APBB1IP HLA-	3.43E-07
lymphocyte p	HLA-DPB1 AIF	3.43E-07
T cell activati	APBB1IP HLA-	3.43E-07
T cell aggrega	APBB1IP HLA-	3.43E-07
lymphocyte a	APBB1IP HLA-	3.43E-07
mononuclear	HLA-DPB1 AIF	3.60E-07
immune syste	CSF1R APBB1	3.60E-07
adaptive imm	C3AR1 C3 C1	3.60E-07
regulation of	HLA-DPB1 AIF	3.60E-07
cell activatio	APBB1IP HLA-	4.65E-07
leukocyte agg	APBB1IP HLA-	4.68E-07
leukocyte pr	HLA-DPB1 AIF	6.15E-07
positive regul	HLA-DPB1 C3	1.21E-06
leukocyte cell	APBB1IP HLA-	1.23E-06
regulation of	HLA-DPB1 AIF	1.93E-06
defense resp	CSF1R HLA-D	6.16E-06
immune effe	APBB1IP C3 T	6.16E-06
homotypic ce	APBB1IP HLA-	6.25E-06
adaptive imm	C3AR1 C3 C1	6.25E-06
positive regul	HLA-DPB1 AIF	6.25E-06
regulation of	HLA-DPB1 C3	9.50E-06
immunoglobu	C3 C1QC C1Q	9.50E-06
regulation of	CSF1R HLA-D	9.50E-06
regulation of	HLA-DPB1 AIF	1.21E-05
T cell prolifer	HLA-DPB1 AIF	1.21E-05
B cell mediat	C3 C1QC C1Q	1.21E-05
regulation of	HLA-DPB1 AIF	1.81E-05
regulation of	HLA-DPB1 AIF	2.80E-05
activation of i	HLA-DPB1 C3	2.85E-05
regulation of	HLA-DPB1 AIF	2.96E-05
lymphocyte m	C3 C1QC C1Q	3.14E-05

tolerance ind	C3AR1 C3 TG	3.71E-05
positive regul	HLA-DPB1 AI	7.79E-05
leukocyte me	C3 VAMP8 C1	8.10E-05
humoral imm	C3 C1QC C1Q	8.30E-05
response to s	CSF1R APBB1	9.16E-05
innate immu	CSF1R HLA-D	9.86E-05
positive regul	HLA-DPB1 AI	9.86E-05
positive regul	HLA-DPB1 AI	0.0001142
negative regu	LST1 INPP5D	0.00012334
negative regu	LST1 INPP5D	0.00012334
positive regul	APBB1IP HLA-	0.00015278
inflammatory	CSF1R C3AR1	0.00019082
cell activatio	APBB1IP TYR	0.00019082
leukocyte act	APBB1IP TYR	0.00019082
regulation of	APBB1IP HLA-	0.00020785
negative regu	LST1 INPP5D	0.00024967
regulation of	HLA-DPB1 AI	0.00026607
positive regul	C3 FCER1G T	0.0002963
positive regul	C3 FCER1G T	0.0002963
regulation of	C3 PTPN6 FC	0.00033485
regulation of	C3 PTPN6 FC	0.00033485
leukocyte mi	C3AR1 AIF1 I	0.00039624
negative regu	LST1 INPP5D	0.00040076
response to	ALOX5 TGFB	0.00048635
positive regul	HLA-DPB1 AI	0.00054306
humoral imm	C3 C1QC C1Q	0.00054588
single organis	APBB1IP HLA-	0.00054588
positive regul	CSF1R HLA-D	0.00054776
lymphocyte a	APBB1IP ADA	0.00068446
regulation of	C3 PTPN6 AD	0.00073013
positive regul	C3 ADA FCER	0.00082756
positive regul	C3 ADA FCER	0.00082756
negative regu	LST1 C1QC IN	0.00087387
negative regu	LST1 INPP5D	0.00093242
myeloid leuk	AIF1 TYROBP	0.00096731
positive regul	C3 VAMP8 CD	0.00108645
regulation of	C3 PTPN6 AD	0.00112863
single organis	APBB1IP HLA-	0.00131058
positive regul	HLA-DPB1 AI	0.00140328
cell-cell adhe	APBB1IP HLA-	0.00142106
complement	C3 C1QC C1Q	0.00168606
positive regul	HLA-DPB1 AI	0.00170282
leukocyte dif	CSF1R TYROB	0.00180845

response to e	FUCA2 C3AR1	0.00180889
negative regu	LST1 INPP5D	0.00204541
response to ii	HLA-DPB1 AIF	0.00216528
T cell activati	APBB1IP LCP1	0.00221055
mammary gla	CSF1R TGFBR	0.00221055
positive regul	HLA-DPB1 AIF	0.00240702
positive regul	HLA-DPB1 AIF	0.00298397
female pregn	UCP2 TGFBR2	0.00360702
positive regul	C3 VAMP8 FC	0.00380138
lymphocyte c	HLA-DPB1 HL	0.00380138
T cell costimu	HLA-DPB1 HL	0.00380138
protein activa	C3 C1QC C1Q	0.00380138
regulation of	CSF1R TYROB	0.00396132
cytokine-mec	CSF1R HLA-DI	0.00398883
regulation of	C3 VAMP8 PT	0.00461329
positive regul	CSF1R APBB1	0.00472442
locomotion	FUCA2 CSF1R	0.00481111
immune resp	HLA-DPB1 C3	0.00521184
positive regul	C3 VAMP8 FC	0.00563221
positive regul	C3AR1 C3 TGI	0.00563221
regulation of	C3 PTPN6 FCE	0.00585025
leukocyte che	C3AR1 AIF1 S	0.00585025
response to c	CSF1R HLA-DI	0.00665043
cell adhesion	APBB1IP HLA-	0.00665043
biological adh	APBB1IP HLA-	0.00665043
antigen proce	HLA-DPB1 HL	0.00665043
antigen proce	HLA-DPB1 HL	0.00665043
response to s	FUCA2 CSF1R	0.00665043
regulation of	CSF1R HLA-DI	0.00665043
immune syste	CSF1R C3AR1	0.00707045
response to e	AIF1 ALOX5 V	0.00733717
negative regu	UCP2 INPP5D	0.00734854
regulation of	CSF1R HLA-DI	0.00734854
multi-organis	FUCA2 VAMP	0.00734854
myeloid denc	TGFBR2 CD37	0.00734854
complement	C3 C1QC C1Q	0.00734854
regulation of	C3AR1 C3 TGI	0.00734854
cellular respo	CSF1R HLA-DI	0.00734854
multi-multice	UCP2 TGFBR2	0.00734854
type IIa hyper	C3 FCER1G	0.00734854
regulation of	C3 FCER1G	0.00734854
positive regul	C3 FCER1G	0.00734854
type II hypers	C3 FCER1G	0.00734854

hypersensitiv	C3 FCER1G	0.00734854
regulation of	C3 FCER1G	0.00734854
positive regul	C3 FCER1G	0.00734854
regulation of	C3 FCER1G	0.00734854
positive regul	C3 FCER1G	0.00734854
common-part	TGFBR2 TGFB	0.00734854
adiponectin-a	ACSL1 ADIPO	0.00734854
cellular respo	HLA-DPB1 AIF	0.00735482
regulation of	CSF1R UCP2 I	0.00735482
cell migration	CSF1R C3AR1	0.00752687
regulation of	INPP5D PTPN	0.00872541
regulation of	APBB1IP C3 V	0.00903442
T cell recepto	HLA-DPB1 HL	0.00933926
positive regul	C3 FCER1G T	0.00968407
neutrophil ch	C3AR1 SPP1 I	0.0101125
secretion by t	VAMP8 AQP1	0.0101125
regulation of	CSF1R INPP5	0.0101125
neutrophil mi	C3AR1 SPP1 I	0.0101125
movement of	CSF1R C3AR1	0.01235043
response to v	APBB1IP AIF1	0.01254372
regulation of	C3 PTPN6 CD	0.01273235
vascular endo	C3AR1 C3 TG	0.01273235
negative regu	PTPN6 VSIG4	0.01273235
antigen proce	HLA-DPB1 HL	0.01273235
response to n	ALOX5 VAMP	0.01273235
positive regul	CSF1R HLA-D	0.0130036
body fluid sec	VAMP8 AQP1	0.01369462
positive regul	CSF1R HLA-D	0.01385
cell motility	CSF1R C3AR1	0.01393481
localization o	CSF1R C3AR1	0.01393481
myeloid leuk	CSF1R TYROB	0.01465182
positive regul	C3AR1 C3 TG	0.01520422
regulation of	C3AR1 AIF1 C	0.01568761
aging	UCP2 TGFBR2	0.01636174
regulation of	CSF1R TYROB	0.01636174
cytokine proc	CSF1R HLA-D	0.01644663
T cell activati	APBB1IP HLA-	0.01644663
acute inflam	C3 FCER1G	0.01644663
tolerance ind	TGFBR2 TGFB	0.01644663
regulation of	C3 FCER1G	0.01644663
positive regul	C3 FCER1G	0.01644663
regulation of	C3 FCER1G	0.01644663
positive regul	C3 FCER1G	0.01644663

lipoxygenase	ALOX5AP ALC	0.01644663
negative regu	C1QC INPP5D	0.01644663
entry of bacte	FUCA2 CAV1	0.01644663
regulation of	FUCA2 CAV1	0.01644663
lipoxin metab	ALOX5AP ALC	0.01644663
interferon-ga	HLA-DPB1 HL	0.01644663
granulocyte c	C3AR1 SPP1 I	0.01644663
granulocyte n	C3AR1 SPP1 I	0.01644663
regulation of	FUCA2 CSF1R	0.01695043
antigen proce	HLA-DPB1 HL	0.01783811
lymphocyte d	TGFBR2 INPP	0.01783811
regulation of	CSF1R TREM2	0.01783811
antigen recep	HLA-DPB1 HL	0.0183248
regulation of	C3 VAMP8 FC	0.01834582
embryo impla	TGFBR2 SPP1	0.01834582
positive regul	INPP5D ADA	0.01834582
glycosyl comp	FUCA2 NAGA	0.01834582
regulation of	CSF1R HLA-D	0.01862696
regulation of	CSF1R C3AR1	0.01889543
cellular respo	CSF1R APBB1	0.01894009
myeloid leuk	C3AR1 AIF1 S	0.01946716
regulation of	CSF1R C3 TRE	0.01983879
gland morpho	CSF1R TGFBR	0.02130707
regulation of	CSF1R HLA-D	0.02179349
positive regul	CD37 FCER1G	0.02238177
dendritic cell	TREM2 TGFB	0.02238177
cellular respo	CSF1R HLA-D	0.02238177
positive regul	C3AR1 AIF1 C	0.02244377
interaction w	FUCA2 VAMP	0.02259612
mammary gla	CSF1R TGFBR	0.02259612
organ regene	UCP2 TGFBR2	0.02259612
positive regul	CSF1R HLA-D	0.02498245
ERK1 and ERK	CSF1R C3 TRE	0.0254019
antigen proce	HLA-DPB1 HL	0.0254678
regulation of	C3 VAMP8 PT	0.026144
regulation of	C3 VAMP8 TG	0.026144
tissue remod	CSF1R INPP5	0.0264678
production of	ALOX5 VAMP	0.02656195
neutrophil ac	TYROBP FCER	0.0270057
complement	C3 VSIG4	0.0270057
glycoside cat	FUCA2 NAGA	0.0270057
negative regu	ADA CRY1	0.0270057
mucus secret	VAMP8 ADA	0.0270057

regulation of	TGFBR2 INPP	0.02762003
cell chemota	C3AR1 AIF1 S	0.02768455
hemopoiesis	CSF1R TYROB	0.02811551
cell surface re	CSF1R HLA-D	0.03043582
homeostatic	CSF1R C3AR1	0.03043582
immune resp	HLA-DPB1 C3	0.0306906
myeloid cell c	CSF1R TYROB	0.0306906
ruffle organiz	CSF1R AIF1 C	0.0306906
regulation of	CSF1R INPP5	0.0306906
long-chain fa	TBXAS1 ALOX	0.03382095
immune resp	HLA-DPB1 C3	0.0353723
hematopoieti	CSF1R TYROB	0.0353723
regulation of	CSF1R C3AR1	0.03629193
regulation of	C3 FCER1G T	0.03629193
negative regu	PTPN6 VSIG4	0.03629193
antigen proce	HLA-DPB1 HL	0.03647703
response to g	AIF1 C3 AQP1	0.03647703
bone remode	CSF1R INPP5	0.03647703
regulation of	C3AR1 AIF1 T	0.03647703
cell proliferat	CSF1R HLA-D	0.03791717
regulation of	C3 VAMP8 IT	0.03802776
antigen proce	HLA-DPB1 HL	0.03902195
unsaturated f	TBXAS1 ALOX	0.03928556
positive regul	CD37 TGFB1	0.03928556
positive regul	C3 FCER1G	0.03928556
glycoside me	FUCA2 NAGA	0.03928556
regulation of	AQP1 SGK1	0.03928556
regulation of	INPP5D PTPN	0.03928556
response to p	C3 TGFB1 CA	0.04062716
cellular respo	AQP1 FNTA C	0.04062716
negative regu	PTPN6 VSIG4	0.04062716
wound healin	APBB1IP C3 T	0.04194068
smooth musc	C3AR1 AIF1 T	0.04280469
response to c	AIF1 C3 AQP1	0.04602997
positive regul	C3 VAMP8 IT	0.04602997
regulation of	CSF1R TYROB	0.04602997
ammonium t	VAMP8 AQP1	0.04602997
positive regul	CSF1R TGFBR	0.04602997
G-protein co	C3AR1 C3 LP	0.04602997
arachidonic a	TBXAS1 ALOX	0.04602997
icosanoid bio	TBXAS1 ALOX	0.04602997
fatty acid der	TBXAS1 ALOX	0.04602997
protein locali	VAMP8 TREM	0.04730251

fatty acid me	TBXAS1 C3 A	0.04739567
monovalent i	VAMP8 UCP2	0.04811368
homeostasis	INPP5D RPS1	0.04811368
gland develo	CSF1R UCP2	0.04919904
protein locali	VAMP8 TRE	0.04919904
positive regul	C3 VAMP8 T	0.04929816
regulation of	CSF1R C3AR1	0.05100304
response to li	AIF1 C3 TRE	0.05100304
regulation of	CSF1R INPP5	0.05100304
histamine se	VAMP8 ADA	0.05100304
regulation of	C1QC INPP5D	0.05100304
positive regul	VAMP8 FCER	0.05100304
neutrophil ac	TYROBP FCER	0.05100304
superoxide a	CYBB TGFB1	0.05100304
positive regul	VAMP8 FCER	0.05100304
defense resp	COTL1 TGFB1	0.05100304
histamine tra	VAMP8 ADA	0.05100304
T cell migrati	AIF1 CXCL16	0.05100304
positive regul	FNTA TGFB1	0.05100304
cellular lipid	CSF1R LPCAT	0.05103986
regulation of	C3 AQP1 SER	0.05198703
regulation of	CSF1R C3AR1	0.05234304
positive regul	C3AR1 C3 TG	0.0556259
entry into ho	FUCA2 VAMP	0.0556259
negative regu	PTPN6 VSIG4	0.0556259
entry into ho	FUCA2 VAMP	0.0556259
positive regul	TGFBR2 INPP	0.0556259
entry into cel	FUCA2 VAMP	0.0556259
entry into ot	FUCA2 VAMP	0.0556259
movement in	FUCA2 VAMP	0.0556259
movement in	FUCA2 VAMP	0.0556259
negative regu	AIF1 SVBP AD	0.0573668
response to c	CSF1R HLA-D	0.06294779
leukocyte ho	ADA FCER1G	0.06294779
regulation of	CD37 FCER1G	0.06294779
positive regul	C3 VAMP8 FC	0.06294779
blood coagul	APBB1IP C3 I	0.06297429
positive regul	CSF1R C3 TRE	0.063496
positive regul	CSF1R TGFBR	0.063496
negative regu	VAMP8 UCP2	0.06374844
response to f	COTL1 TGFB1	0.06422831
positive regul	VAMP8 FCER	0.06422831
granulocyte a	TYROBP FCER	0.06422831

myeloid denc	TGFBR2 TGFB	0.06422831
positive regul	VAMP8 FCER	0.06422831
regulation of	PTPN6 ADA	0.06422831
hemostasis	APBB1IP C3 I	0.06504531
coagulation	APBB1IP C3 I	0.06504531
unsaturated f	TBXAS1 ALOX	0.06840837
B cell differer	INPP5D PTPN	0.06840837
negative regu	INPP5D PTPN	0.06840837
negative regu	AIF1 SVBP AD	0.06961733
response to c	CSF1R HLA-D	0.07037764
T cell differen	TGFBR2 ADA	0.07161651
regulation of	CSF1R VAMP	0.07289896
myeloid cell a	TYROBP VAM	0.07566438
lipid storage	C3 CRY1 CAV	0.07566438
bone resorpti	CSF1R INPP5	0.07566438
regulation of	CSF1R TYROB	0.07566438
negative regu	C3 AQP1 SER	0.07621886
apoptotic pro	AIF1 UCP2 PC	0.07948082
inflammatory	C3 FCER1G	0.07948082
regulation of	CD37 TGFB1	0.07948082
leukotriene b	ALOX5AP ALC	0.07948082
positive regul	TREM2 ADA	0.07948082
peptidyl-tyro	CSF1R TREM	0.07948082
peptidyl-tyro	CSF1R TREM	0.08245686
myeloid leuk	C3 VAMP8 FC	0.08245686
regulation of	VAMP8 TREM	0.08245686
regulation of	VAMP8 TREM	0.08245686
symbiosis, en	FUCA2 VAMP	0.08392277
interspecies i	FUCA2 VAMP	0.08392277
programmed	AIF1 UCP2 PC	0.08485363
negative regu	C3 AQP1 SER	0.08507905
B cell activati	INPP5D PTPN	0.08507905

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0001580	8.59E-05	256.666667	0.01529052	2	5
GO:0050912	0.00012863	192.454545	0.01834862	2	6
GO:0050913	0.00012863	192.454545	0.01834862	2	6
GO:0050907	0.00056013	76.8727273	0.03669725	2	12
GO:0050909	0.00066083	69.8677686	0.03975535	2	13
GO:0009593	0.0019269	38.3454545	0.06727829	2	22
GO:0050906	0.00290273	30.64	0.08256881	2	27
GO:0009753	0.0030581	Inf	0.0030581	1	1
GO:0030638	0.0030581	Inf	0.0030581	1	1
GO:0030647	0.0030581	Inf	0.0030581	1	1
GO:0036158	0.0030581	Inf	0.0030581	1	1
GO:0044313	0.0030581	Inf	0.0030581	1	1
GO:0044597	0.0030581	Inf	0.0030581	1	1
GO:0044598	0.0030581	Inf	0.0030581	1	1
GO:0060060	0.0030581	Inf	0.0030581	1	1
GO:0070593	0.0030581	Inf	0.0030581	1	1
GO:0071395	0.0030581	Inf	0.0030581	1	1
GO:0071798	0.0030581	Inf	0.0030581	1	1
GO:0071799	0.0030581	Inf	0.0030581	1	1
GO:0007606	0.00485313	23.1680441	0.10703364	2	35
GO:0036159	0.00610757	353.083333	0.00611621	1	2
GO:0060287	0.00610757	353.083333	0.00611621	1	2
GO:0070286	0.00610757	353.083333	0.00611621	1	2
GO:0090267	0.00610757	353.083333	0.00611621	1	2
GO:0035871	0.00914843	176.5	0.00917431	1	3
GO:0044458	0.00914843	176.5	0.00917431	1	3
GO:0045579	0.00914843	176.5	0.00917431	1	3
GO:0090232	0.00914843	176.5	0.00917431	1	3

Term	Genes	padjust
detection of c	TAS2R4 TAS2	0.02486806
detection of c	TAS2R4 TAS2	0.02486806
sensory perce	TAS2R4 TAS2	0.02486806
detection of c	TAS2R4 TAS2	0.07665609
sensory perce	TAS2R4 TAS2	0.07665609
detection of c	TAS2R4 TAS2	0.09335265
detection of s	TAS2R4 TAS2	0.09335265
response to ja	AKR1C2	0.09335265
polyketide me	AKR1C2	0.09335265
aminoglycosid	AKR1C2	0.09335265
outer dynein	LRRC6	0.09335265
protein K6-lin	OTUD3	0.09335265
daunorubicin	AKR1C2	0.09335265
doxorubicin r	AKR1C2	0.09335265
post-embryon	DSCAM	0.09335265
dendrite self-	DSCAM	0.09335265
cellular respo	AKR1C2	0.09335265
response to p	AKR1C2	0.09335265
cellular respo	AKR1C2	0.09335265
sensory perce	TAS2R4 TAS2	0.14074068
inner dynein a	LRRC6	0.14759969
epithelial ciliu	LRRC6	0.14759969
axonemal dyn	LRRC6	0.14759969
positive regul	PCID2	0.14759969
protein K11-li	OTUD3	0.1895032
motile cilium	LRRC6	0.1895032
positive regul	PCID2	0.1895032
positive regul	PCID2	0.1895032

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0006865	0.00064198	23.3563433	0.18113385	3	70
GO:0003333	0.00221844	36.017094	0.07245354	2	28
GO:0046942	0.00232899	14.625	0.28205128	3	109
GO:0015849	0.00239088	14.4848131	0.28463891	3	110
GO:0002949	0.00258763	Inf	0.00258763	1	1
GO:0015734	0.00258763	Inf	0.00258763	1	1
GO:0061402	0.00258763	Inf	0.00258763	1	1
GO:0070525	0.00258763	Inf	0.00258763	1	1
GO:1903825	0.00428178	25.2432432	0.10091743	2	39
GO:0015711	0.00514275	10.9015957	0.37261821	3	144
GO:0006867	0.00516916	423.9	0.00517525	1	2
GO:0006868	0.00516916	423.9	0.00517525	1	2
GO:0015817	0.00516916	423.9	0.00517525	1	2
GO:0051365	0.00516916	423.9	0.00517525	1	2
GO:0089709	0.00516916	423.9	0.00517525	1	2
GO:1902024	0.00516916	423.9	0.00517525	1	2
GO:0015802	0.00774463	211.9	0.00776288	1	3
GO:0060907	0.00774463	211.9	0.00776288	1	3
GO:0071468	0.00774463	211.9	0.00776288	1	3

Term
amino acid transport
amino acid transmembrane transport
carboxylic acid transport
organic acid transport
tRNA threonylcarbamoyladenosine modification
taurine transport
positive regulation of transcription from RNA polymerase II promoter in response to acidic pH
tRNA threonylcarbamoyladenosine metabolic process
organic acid transmembrane transport
organic anion transport
asparagine transport
glutamine transport
histidine transport
cellular response to potassium ion starvation
L-histidine transmembrane transport
L-histidine transport
basic amino acid transport
positive regulation of macrophage cytokine production
cellular response to acidic pH

Genes	padjust
SLC6A12 SLC6	0.11889078
SLC6A6 SLC38	0.11889078
SLC6A12 SLC6	0.11889078
SLC6A12 SLC6	0.11889078
OSGEPL1	0.11889078
SLC6A6	0.11889078
SLC38A3	0.11889078
OSGEPL1	0.11889078
SLC6A6 SLC38	0.11889078
SLC6A12 SLC6	0.11889078
SLC38A3	0.11889078
SLC38A3	0.11889078
SLC38A3	0.11889078
SLC38A3	0.11889078
SLC38A3	0.11889078
SLC38A3	0.11889078
SLC38A3	0.15000119
SEMA7A	0.15000119
SLC38A3	0.15000119

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0009753	0.002352388	Inf	0.00235239	1	1
GO:0030638	0.002352388	Inf	0.00235239	1	1
GO:0030647	0.002352388	Inf	0.00235239	1	1
GO:0033085	0.002352388	Inf	0.00235239	1	1
GO:0038110	0.002352388	Inf	0.00235239	1	1
GO:0038161	0.002352388	Inf	0.00235239	1	1
GO:0042505	0.002352388	Inf	0.00235239	1	1
GO:0042512	0.002352388	Inf	0.00235239	1	1
GO:0042525	0.002352388	Inf	0.00235239	1	1
GO:0042527	0.002352388	Inf	0.00235239	1	1
GO:0044597	0.002352388	Inf	0.00235239	1	1
GO:0044598	0.002352388	Inf	0.00235239	1	1
GO:0060339	0.002352388	Inf	0.00235239	1	1
GO:0070103	0.002352388	Inf	0.00235239	1	1
GO:0070104	0.002352388	Inf	0.00235239	1	1
GO:0070669	0.002352388	Inf	0.00235239	1	1
GO:0071352	0.002352388	Inf	0.00235239	1	1
GO:0071395	0.002352388	Inf	0.00235239	1	1
GO:0071798	0.002352388	Inf	0.00235239	1	1
GO:0071799	0.002352388	Inf	0.00235239	1	1
GO:1902202	0.002352388	Inf	0.00235239	1	1
GO:1902205	0.002352388	Inf	0.00235239	1	1
GO:1902206	0.002352388	Inf	0.00235239	1	1
GO:1902211	0.002352388	Inf	0.00235239	1	1
GO:1902212	0.002352388	Inf	0.00235239	1	1
GO:1902214	0.002352388	Inf	0.00235239	1	1
GO:1902215	0.002352388	Inf	0.00235239	1	1
GO:1902227	0.002352388	Inf	0.00235239	1	1
GO:1902232	0.002352388	Inf	0.00235239	1	1
GO:1902233	0.002352388	Inf	0.00235239	1	1
GO:1903899	0.002352388	Inf	0.00235239	1	1
GO:1903970	0.002352388	Inf	0.00235239	1	1
GO:1903973	0.002352388	Inf	0.00235239	1	1
GO:2000399	0.002352388	Inf	0.00235239	1	1
GO:2000586	0.002352388	Inf	0.00235239	1	1
GO:2000587	0.002352388	Inf	0.00235239	1	1
GO:0035771	0.004699794	471.111111	0.00470478	1	2
GO:0042524	0.004699794	471.111111	0.00470478	1	2
GO:0045650	0.004699794	471.111111	0.00470478	1	2
GO:0060331	0.004699794	471.111111	0.00470478	1	2

GO:0060336	0.004699794	471.111111	0.00470478	1	2
GO:1900103	0.004699794	471.111111	0.00470478	1	2
GO:1902226	0.004699794	471.111111	0.00470478	1	2
GO:1902237	0.004699794	471.111111	0.00470478	1	2
GO:1903969	0.004699794	471.111111	0.00470478	1	2
GO:1903972	0.004699794	471.111111	0.00470478	1	2
GO:0036297	0.007042228	235.5	0.00705716	1	3
GO:0038145	0.007042228	235.5	0.00705716	1	3
GO:0042518	0.007042228	235.5	0.00705716	1	3
GO:0043368	0.007042228	235.5	0.00705716	1	3
GO:0045059	0.007042228	235.5	0.00705716	1	3
GO:1903897	0.007042228	235.5	0.00705716	1	3
GO:0010804	0.009379699	156.962963	0.00940955	1	4
GO:0035791	0.009379699	156.962963	0.00940955	1	4
GO:0042448	0.009379699	156.962963	0.00940955	1	4
GO:0042506	0.009379699	156.962963	0.00940955	1	4
GO:0042508	0.009379699	156.962963	0.00940955	1	4
GO:0042510	0.009379699	156.962963	0.00940955	1	4
GO:0042522	0.009379699	156.962963	0.00940955	1	4
GO:0042532	0.009379699	156.962963	0.00940955	1	4
GO:0045581	0.009379699	156.962963	0.00940955	1	4
GO:0048012	0.009379699	156.962963	0.00940955	1	4
GO:0070102	0.009379699	156.962963	0.00940955	1	4
GO:1900101	0.009379699	156.962963	0.00940955	1	4

Term
response to jasmonic acid
polyketide metabolic process
aminoglycoside antibiotic metabolic process
negative regulation of T cell differentiation in thymus
interleukin-2-mediated signaling pathway
prolactin signaling pathway
tyrosine phosphorylation of Stat6 protein
negative regulation of tyrosine phosphorylation of Stat1 protein
regulation of tyrosine phosphorylation of Stat6 protein
negative regulation of tyrosine phosphorylation of Stat6 protein
daunorubicin metabolic process
doxorubicin metabolic process
negative regulation of type I interferon-mediated signaling pathway
regulation of interleukin-6-mediated signaling pathway
negative regulation of interleukin-6-mediated signaling pathway
response to interleukin-2
cellular response to interleukin-2
cellular response to jasmonic acid stimulus
response to prostaglandin D
cellular response to prostaglandin D stimulus
regulation of hepatocyte growth factor receptor signaling pathway
regulation of interleukin-2-mediated signaling pathway
negative regulation of interleukin-2-mediated signaling pathway
regulation of prolactin signaling pathway
negative regulation of prolactin signaling pathway
regulation of interleukin-4-mediated signaling pathway
negative regulation of interleukin-4-mediated signaling pathway
negative regulation of macrophage colony-stimulating factor signaling pathway
regulation of positive thymic T cell selection
negative regulation of positive thymic T cell selection
positive regulation of PERK-mediated unfolded protein response
negative regulation of response to macrophage colony-stimulating factor
negative regulation of cellular response to macrophage colony-stimulating factor stimulus
negative regulation of thymocyte aggregation
regulation of platelet-derived growth factor receptor-beta signaling pathway
negative regulation of platelet-derived growth factor receptor-beta signaling pathway
interleukin-4-mediated signaling pathway
negative regulation of tyrosine phosphorylation of Stat5 protein
negative regulation of macrophage differentiation
negative regulation of response to interferon-gamma

negative regulation of interferon-gamma-mediated signaling pathway
positive regulation of endoplasmic reticulum unfolded protein response
regulation of macrophage colony-stimulating factor signaling pathway
positive regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway
regulation of response to macrophage colony-stimulating factor
regulation of cellular response to macrophage colony-stimulating factor stimulus
interstrand cross-link repair
macrophage colony-stimulating factor signaling pathway
negative regulation of tyrosine phosphorylation of Stat3 protein
positive T cell selection
positive thymic T cell selection
regulation of PERK-mediated unfolded protein response
negative regulation of tumor necrosis factor-mediated signaling pathway
platelet-derived growth factor receptor-beta signaling pathway
progesterone metabolic process
tyrosine phosphorylation of Stat5 protein
tyrosine phosphorylation of Stat1 protein
regulation of tyrosine phosphorylation of Stat1 protein
regulation of tyrosine phosphorylation of Stat5 protein
negative regulation of tyrosine phosphorylation of STAT protein
negative regulation of T cell differentiation
hepatocyte growth factor receptor signaling pathway
interleukin-6-mediated signaling pathway
regulation of endoplasmic reticulum unfolded protein response

Genes	padjust
AKR1C2	0.04077472
AKR1C2	0.04077472
AKR1C2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
AKR1C2	0.04077472
AKR1C2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
AKR1C2	0.04077472
AKR1C2	0.04077472
AKR1C2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.04077472
PTPN2	0.06375372
PTPN2	0.06375372
PTPN2	0.06375372
PTPN2	0.06375372

PTPN2	0.06375372
PTPN2	0.06375372
PTPN2	0.06375372
PTPN2	0.06375372
PTPN2	0.06375372
PTPN2	0.06375372
POLN	0.08450673
PTPN2	0.08450673
PTPN2	0.08450673
PTPN2	0.08450673
PTPN2	0.08450673
PTPN2	0.08450673
PTPN2	0.09145207
PTPN2	0.09145207
AKR1C2	0.09145207
PTPN2	0.09145207
PTPN2	0.09145207
PTPN2	0.09145207
PTPN2	0.09145207
PTPN2	0.09145207
PTPN2	0.09145207
PTPN2	0.09145207
PTPN2	0.09145207
PTPN2	0.09145207

UP	MA	iLBD	PD	DLB
RNU11	-1.9309134	-1.6617822	-1.7374788	5.33017443
TMPRSS5	-1.3325065	-1.1140569	-1.1661592	3.61272265
AZGP1	0	-1.9207174	-1.5796661	3.50038349
SNORA14A	-1.212116	-1.3254479	-0.8749352	3.41249909
SNORA54	-0.8657434	-1.3032692	-0.9428167	3.11182927
OR7A5	0	-1.5754752	-1.3864719	2.96194711
KIF1C	-0.7294888	-1.1182292	-1.0180411	2.86575911
ID3	-0.7785519	-1.0968958	-0.9894194	2.86486706
NUPR1	-1.2077225	-1.62229	0	2.83001252
LRP2	0	-1.4629576	-1.3572525	2.82021009
CA2	-0.6448751	-1.2165509	-0.9201254	2.78155134
P2RX7	-0.8617466	-0.9634775	-0.9518927	2.77711682
MID1IP1	0	-1.5094841	-1.2593223	2.7688064
IL17RB	-1.0134778	-0.791836	-0.9143385	2.71965231
SLC5A11	0	-1.3720726	-1.2147632	2.58683584
FAM38B2	0	-1.2051322	-1.3451414	2.55027355
RFTN2	-0.7142814	-0.9368717	-0.8875015	2.53865462
KLF15	-0.7827034	-0.8351562	-0.9147136	2.53257315
SNORA62	-1.3882302	0	-1.0753855	2.46361569
FAM38B	0	-1.2160255	-1.2417981	2.45782366
PRKX	-0.7629644	-0.9072951	-0.7838409	2.45410041
MT1G	-0.6843848	-1.0373562	-0.7307421	2.45248306
PRELP	-0.8928918	-0.8817665	-0.6638325	2.4384908
OR2M5	0	2.4305734	-1.3521395	-1.0784339
SNORA75	-1.3598257	0	-1.0430651	2.40289081
SNORD6	-0.7768868	-0.9627974	-0.6475091	2.38719323
MYOT	0	-1.2499591	-1.1356979	2.385657
MIR186	-1.1475082	2.36065001	0	-1.2131418
PGCP	-0.6859194	-0.8886762	-0.7808614	2.35545695
MIR221	-0.9259035	2.3138816	-0.7141699	-0.6738082
OR2M3	0	2.30772144	-1.2025364	-1.1051851
HIGD1B	-0.762922	-0.7209654	-0.8200711	2.30395848
GPR146	-0.6215083	-0.9051602	-0.7676719	2.29434036
OR2M4	0	2.28783078	-1.1989727	-1.0888581
LOC121952	-1.0876582	2.27350994	0	-1.1858517
SNORA20	-0.7529143	-0.9701565	-0.5410693	2.26414002
NKX6-2	0	-1.1497499	-1.1119367	2.26168658
UIMC1	0	-1.2496135	-1.0067289	2.25634241
MT1P3	-0.6149397	-0.8666858	-0.7731754	2.25480094
NACC2	-0.5660007	-0.8799505	-0.7754106	2.2213619
SLC7A2	0	-1.2907957	-0.9165313	2.20732699
PPAP2C	0	-1.07693	-1.1285054	2.20543544
ARRDC2	0	-1.2307001	-0.9405049	2.17120502
TGFB3	0	-1.180229	-0.9761888	2.15641777

OR2L3	-0.7154403	2.14823557	-0.6662712	-0.7665241
C18orf58	0	-1.0926213	-1.0549982	2.14761944
SNORD95	-0.567697	-0.9307118	-0.6367649	2.13517364
AKR1C3	-0.7220311	-0.7146612	-0.6975271	2.1342194
SNORA6	-0.7986132	-0.78244	-0.5102231	2.09127631
PDK4	0	-1.034877	-0.9956921	2.03056904

DOWN	MA	iLBD	PD	DLB
C3	1.59767282	[redacted]	1.58326291	1.73479645
ALOX5AP	1.68127021	[redacted]	1.51497346	1.54345527
C1QB	1.56497269	[redacted]	1.64958925	1.46219462
NRIP3	1.48227515	1.60512476	1.57034937	[redacted]
HLA-DRA	1.63638817	[redacted]	1.47938871	1.52565825
C20orf103	1.37476902	1.47864332	1.55192389	[redacted]
C1QC	1.4704506	[redacted]	1.47654047	1.45755775
MAL2	1.33898643	1.46999915	1.51436203	[redacted]
PCSK1	1.3535657	1.58130018	1.3472462	[redacted]
MAS1	1.3130034	1.53444953	1.41035831	[redacted]
GABRA1	1.40140342	1.3940116	1.41500905	[redacted]
HTR2A	1.28600126	1.44500042	1.40701631	[redacted]
RBP4	1.27881941	1.3187837	1.5388241	[redacted]
RPH3A	1.31850397	1.56991504	1.22777631	[redacted]
INA	1.31390114	1.40545274	1.33128974	[redacted]
RAB3C	1.27563662	1.31647455	1.40436545	[redacted]
LCP1	1.36471909	-3.9853657	1.31523279	1.30541385
ANO3	1.28001064	1.27759097	1.39191779	[redacted]
LAPTM5	1.47870928	[redacted]	1.22380503	1.24205374
GAD2	1.38020415	1.20551837	1.35432512	[redacted]
HCN1	1.24863747	1.37428454	1.30951234	[redacted]
SV2C	1.36658263	1.40819862	1.08871925	[redacted]
STAT4	1.13852091	1.42654981	1.25117306	[redacted]
GFRA2	1.09460886	1.44392752	1.23079509	[redacted]
CALB2	1.0625505	1.22263186	1.47497675	[redacted]
GABRG2	1.1953713	1.27386544	1.28901729	[redacted]
CALB1	1.65587882	0	2.05741561	[redacted]
B4GALT6	1.19258828	1.24916159	1.16567029	[redacted]
RAB27B	1.00704779	1.16419966	1.43484544	[redacted]
CAMK1G	1.15676859	1.15333237	1.21023825	[redacted]
GPR34	1.2603932	-3.5084384	1.13720208	1.11084316
HLA-DPB1	1.29413551	-3.4834118	1.10359141	1.08568483
C2orf80	1.05067778	1.12213318	1.29281419	-3.4656252
CSF1R	1.29188684	-3.4164752	0.97132758	1.15326078
FGF9	1.02844933	1.3353039	1.04432361	[redacted]
CD74	1.13429033	-3.3987988	1.08703048	1.17747802
PART1	0.85382849	1.36905196	1.1568038	[redacted]
NCALD	1.17409078	1.14403946	1.06150485	[redacted]
RGS4	1.03200372	1.23793778	1.07516034	[redacted]
CBLN4	1.00586628	1.147557	1.18516852	[redacted]
PCP4	1.13492027	1.11170093	1.08369028	[redacted]
VSIG4	0	-3.3255216	1.64024768	1.68527394
OR14I1	0.91747473	1.26408467	1.13826856	[redacted]
GABRA4	0.95719036	1.13945463	1.18841487	[redacted]

KCNIP4	0.89154446	1.23748036	1.14718924	[redacted]
PVALB	1.6202915	1.64900306	0	[redacted]
KCNC2	1.00380065	1.14775798	1.11495764	[redacted]
GABRA3	0.97414359	1.02224831	1.26857089	[redacted]
NRN1	1.07053005	1.12036832	1.06847015	[redacted]
ENTPD3	1.14150557	1.02369643	1.071376	[redacted]

Table V: Top 20 hub genes per modules

M3-green	M4-lightcyan	M5-brown	M6-tan	M9-salmon	M10-darkred
LOC730153	MSN	ATP6V1B2	LAPTM5	STIP1	UGT2B11
NPIPL2	TAGLN2	ARHGEF9	PTPRC	AHSA1	UGT2B10
LOC728888	CLIC1	HPRT1	NCKAP1L	CHORDC1	OR11H1..OR11
NPIPL3	TIMP1	ATP6V1A	CD68	SERPINH1	OR2J3
NPIP	PLP2	GOT1	VAMP8	DNAJA1	OR4M1
LOC728741	TNFRSF1A	B4GALT6	CD74	JMJD6	OR4F17..OR4F
LOC729602	CSDA	CDK5	FCER1G	MKNK2	BAGE..BAGE3
LOC348162	CD44	NAP1L3	LAIR1	DNAJB1	OR4K2
PDXDC2	OSMR	DCLK1	C1QB	PLOD1	CWH43
LOC613037	FSTL1..MIR198	NRIP3	ALOX5AP	IFRD1	YIF1A
LOC10028844	SERPINA3	NAPB	MS4A6A	HIST1H4B	CTBS
LOC10013224	TMBIM1	GRIA3	SCIN	HSPE1	AHR
LOC729978	STAT3	C2orf80	HLA.DRA	HSPD1	LOC442421..L
LOC339047	ANXA2	ELMOD1	TYROBP	P4HA1	PANX2
LOC399491	EMP1	MAL2	FYB	HSPA1A..HSP	C17orf51
LOC10028833	CNN3	RGS7	S100A11	XPO1	LOC729724
HYDIN2	PLSCR1	WDR47	ARHGDIB	MLKL	SNORD109A..S
LOC10028829	TP53	SLC9A6	C1QC	DNAJB4	POU6F2
PKD1P1	BEST3	SCG5	CD4	HIST1H4H	LOC730144
PKD1	GBP3	ST8SIA3	CYBB	ZNF473	KIF21B

M11-royalblue	M7-midnightblue
LOC100289454	PPP1R15A
RP11.195B21.3	EGR2
CCDC29	CYR61
LOC100289352	RGS2
ANKRD20B	NPAS4
LOC100289026	FOSB
LRRC37A2..LRR	PTGS2
ANKRD20A1..A	MIR7.3
LOC644397	EGR4
LOC100294342	ARPM1
LOC100294335.	C2orf66
LOC100127950	ARC
TAS2R4	CXCL9
SNORD116.28	ZFAND2A
PLGLA..PLGLB1.	ATP13A4
PAR5..SNORD64	JUNB
SLC38A11	RANBP3L
RNF148	JUN
TAS2R50	HSPH1
SYCP2	NR4A3

InputCategories
blue
blue
blue
blue
blue
blue
blue
blue
blue
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown
brown

brown
brown
brown
brown
brown
brown
cyan
cyan
cyan
cyan
cyan
cyan
cyan
cyan
green
lightcyan
lightcyan
lightcyan
lightcyan
lightcyan
lightcyan
lightcyan
lightyellow
midnightblue
midnightblue
salmon
salmon
tan
tan
tan
tan
tan
tan
tan
tan

UserDefinedCategories	Type
blue_M2_Oligodendrocytes__HumanMeta	Brain
turquoise_M9_Oligodendrocyte__CTX	Brain
Oligodendrocyte_probable__Cahoy	Brain
tan_noChangeAD_oligo_plasmaMembrane__Blalock_AD	Brain
turquoise_upAging_oligo__Lu_Aging	Brain
Oligodendrocyte_definite__Cahoy	Brain
Oligodendrocyte__ABA	Brain
black_WhiteMatter__HumanChimp	Brain
blue_downAD_metalIonTransport_glycoprotein__Blalock_AD	Brain
Neuron_probable__Cahoy	Brain
DownWithAlzheimers_Blalock__ADvsCT_inCA1	Brain
red_M11_Neuron__HumanMeta	Brain
DownWithAlzheimers_Liang__ADvsCT_inCA1	Brain
PostSynapticDensity_proteins__Bayes	Brain
brown_downAD_mitochondrion__Blalock_AD	Brain
blue_M16_Neuron__CTX	Brain
blue_downAging_mitochondria_synapse__Lu_Aging	Brain
Autism_associated_module_M12__Voineagu	Brain
Neuron_definite__Cahoy	Brain
purple_downAD_synapticTransmission__Blalock_AD	Brain
brown_Cortex__HumanChimp	Brain
blue_Cortex__HumanChimp	Brain
pink_downAD_synapticTransmission__Blalock_AD	Brain
yellow_M18__CTX	Brain
PresynapticCompartmentProteins_Morciano__MO	Brain
Neuron__ABA	Brain
black_M1_PvalbInterneurons__HumanMeta	Brain
turquoise_M14_Nucleus__MouseMeta	Brain
green_M5_Mitochondria__HumanMeta	Brain
tan_M13_Neuron__MouseMeta	Brain
tan_M13_Neuron__HumanMeta	Brain
turquoise_CingulateNeurons(allTypes)/Layer5__Sugino/Winden	Brain
magenta_downAD_synapticTransmission__Blalock_AD	Brain
greenyellow_downAD_ionAndCalciumTransport__Blalock_AD	Brain
black_M11__CTX	Brain
GlutamatergicNeuronsInMouseCortex_Sugino__MO	Brain
CA3specific_Newrzella__CA1vsCA3	Brain
Autism_differential_expression_across_at_least_one_comparison__Voineagu	Brain
brown_pyramidalNeurons_Layer5/basolateralAmygdala__Sugino/Winden	Brain
turquoise_Cerebellum__HumanChimp	Brain

Synaptic__MitochondrialType	Brain
blue_downAD_metalIonTransport_glycoprotein__Blalock_AD	Brain
green_M10_GlutamatergicSynapticFunction__CTX	Brain
brown_M15_Astrocyte__CTX	Brain
Autism_susceptability_genes_from_Pinto_et_al_2010__Voineagu	Brain
turquoise_downAD_intracellularTransport_cytoskeleton__Blalock_AD	Brain
Neuron_probable__Cahoy	Brain
Autism_associated_module_M12__Voineagu	Brain
PostSynapticDensity_proteins__Bayes	Brain
blue_downAD_metalIonTransport_glycoprotein__Blalock_AD	Brain
turquoise_Cerebellum__HumanChimp	Brain
greenyellow_M6_GlutatmatergicSynapse__MouseMeta	Brain
green_M10_GlutamatergicSynapticFunction__CTX	Brain
turquoise_M14_Nucleus__HumanMeta	Brain
turquoise_M14_Nucleus__HumanMeta	Brain
magenta_M8_Microglia(Type2)__HumanMeta	Brain
orange_M5_Microglia(Type2)__CTX	Brain
Astrocyte_probable__Cahoy	Brain
Autism_differential_expression_across_at_least_one_comparison__Voineagu	Brain
UpWithAlzheimers_Blalock__ADvsCT_inCA1	Brain
upActivationMicroglia_3treatments_Thomas__MicrogialMarkers	Brain
Up_CD40_stimulation_in_MG_AitGhezala__MicrogialMarkers	Brain
palegreen_M1_Gender__CTX	Brain
tan_M12_Hypoxia__CTX	Brain
magenta_M8_Microglia(Type2)__MouseMeta	Brain
black_noChangeAD_heatShockProteinActivity__Blalock_AD	Brain
magenta_M8_Microglia(Type2)__MouseMeta	Brain
pink_M10_Microglia(Type1)__HumanMeta	Brain
purple_M4_Microglia(Type1)__CTX	Brain
upInFrontalCortex__EarlyAD	Brain
upInHippocampus__EarlyAD	Brain
orange_M5_Microglia(Type2)__CTX	Brain
upMGactivagtion_GSE1910__MicrogialMarkers	Brain
mutationMouseOrHumanOrBoth__JAXdiseaseGene	Brain
mutationHuman__JAXdiseaseGene	Brain

CorrectedPvalues
1.86E-171
1.48E-100
6.05E-88
2.76E-53
6.88E-49
6.11E-36
2.02E-23
1.15E-17
0.008322441
4.44E-83
3.74E-73
3.56E-52
5.90E-49
1.00E-47
7.77E-43
4.84E-36
1.27E-34
4.16E-31
1.22E-25
4.44E-24
8.28E-24
8.58E-21
2.36E-17
2.47E-17
2.22E-15
5.55E-15
8.87E-14
1.04E-13
1.60E-12
4.54E-10
8.17E-10
3.27E-08
3.30E-07
1.96E-06
3.63E-06
1.83E-05
5.84E-05
0.001032945
0.00119358
0.001545722

0.00638425
0.007125222
0.007316455
0.015941957
0.019795833
0.031021172
1.09E-09
7.85E-05
0.001065916
0.001732595
0.001900391
0.012301844
0.042173636
0.046944889
0.000797992
1.98E-38
7.46E-23
2.12E-11
2.06E-06
0.000315952
0.038481109
0.043310216
1.26E-10
4.60E-16
0.02671702
1.37E-22
7.97E-06
2.62E-95
3.81E-22
4.84E-22
3.16E-06
4.55E-06
5.65E-06
0.000554951
0.002772801

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0019853	0.0001994	Inf	0.02847651	2	2
GO:0071103	0.00190992	8.65546218	0.54105363	4	38
GO:0048193	0.00276505	5.80965909	0.98243949	5	69
GO:0006886	0.00384163	2.88394558	4.42809682	11	311
GO:0019852	0.00399898	28.6137931	0.09966777	2	7
GO:0035036	0.00399898	28.6137931	0.09966777	2	7
GO:0042364	0.00399898	28.6137931	0.09966777	2	7
GO:0000375	0.00452905	6.67207792	0.68343617	4	48
GO:0000377	0.00452905	6.67207792	0.68343617	4	48
GO:0000398	0.00452905	6.67207792	0.68343617	4	48
GO:1903308	0.00505144	9.88516746	0.35595634	3	25
GO:1902275	0.00629585	9.05701754	0.38443284	3	27
GO:0009988	0.00673079	20.4285714	0.12814428	2	9
GO:0016482	0.00832166	2.69477352	4.22876127	10	297

Term
L-ascorbic acid biosynthetic process
DNA conformation change
Golgi vesicle transport
intracellular protein transport
L-ascorbic acid metabolic process
sperm-egg recognition
water-soluble vitamin biosynthetic process
RNA splicing, via transesterification reactions
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
mRNA splicing, via spliceosome
regulation of chromatin modification
regulation of chromatin organization
cell-cell recognition
cytoplasmic transport

Genes	padjust
AKR1A1 GSTO1	0.33937264
ASF1A RECQL SMC2 TOP3B	0.50486474
AP1G2 COPZ1 LYPLA1 MACF1 SNX2	0.50486474
AP1G2 C11orf73 COPZ1 EMD KAT2A LYPLA1 MACF1 RAB7A RABL3 SNX2 VPS25	0.50486474
AKR1A1 GSTO1	0.50486474
ADAM20 CATSPER2	0.50486474
AKR1A1 GSTO1	0.50486474
LSM3 RSRC1 SNRNP70 TRA2A	0.50486474
LSM3 RSRC1 SNRNP70 TRA2A	0.50486474
LSM3 RSRC1 SNRNP70 TRA2A	0.50486474
ASF1A FLCN KAT2A	0.50486474
ASF1A FLCN KAT2A	0.50486474
ADAM20 CATSPER2	0.50486474
C11orf73 EMD GSTO1 KAT2A LYPLA1 MACF1 RAB7A RSRC1 SNX2 VPS25	0.50486474

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0006954	2.64E-08	6.96197843	3.01352634	16	153
GO:0006950	1.79E-07	3.24486868	21.0946844	43	1071
GO:0006952	1.05E-06	3.69073276	9.00118652	25	457
GO:0002526	1.26E-06	16.4508009	0.59088752	7	30
GO:0098602	3.15E-06	4.69373134	4.25439013	16	216
GO:0044092	4.43E-06	3.99120411	6.00735643	19	305
GO:0050896	5.17E-06	3.01165569	44.2180826	64	2245
GO:0070887	8.25E-06	2.87626459	15.8357855	33	804
GO:0034097	8.80E-06	4.52550551	4.07712387	15	207
GO:0043086	1.24E-05	4.1652452	4.72710014	16	240
GO:0009605	2.86E-05	2.76013849	14.4373517	30	733
GO:0012501	3.46E-05	2.93494557	10.9117228	25	554
GO:0008219	3.56E-05	2.87893184	11.6404841	26	591
GO:0016265	3.56E-05	2.87893184	11.6404841	26	591
GO:0043207	3.58E-05	4.18544654	4.03773137	14	205
GO:0051707	3.58E-05	4.18544654	4.03773137	14	205
GO:0034109	3.84E-05	5.15079365	2.56051258	11	130
GO:0071345	4.15E-05	4.38086735	3.56502136	13	181
GO:0019079	4.17E-05	16.4863782	0.41362126	5	21
GO:0009607	4.69E-05	4.07349896	4.13621262	14	210
GO:0042981	4.74E-05	3.12468061	8.3709065	21	425
GO:0098542	4.80E-05	5.52191781	2.16658757	10	110
GO:0043067	5.45E-05	3.09072581	8.4496915	21	429
GO:0019221	5.84E-05	4.89622222	2.67869008	11	136
GO:0007159	6.53E-05	5.30426765	2.24537257	10	114
GO:0010033	8.13E-05	2.52967448	16.8009018	32	853
GO:0006915	8.84E-05	2.79399516	10.8132416	24	549
GO:0002376	0.00010035	2.63969436	13.0980066	27	665
GO:0002252	0.00010041	3.98377329	3.88016137	13	197
GO:0016337	0.00010041	3.98377329	3.88016137	13	197
GO:0051346	0.00010044	5.58768428	1.91053631	9	97
GO:0010212	0.0001261	9.11910946	0.80754627	6	41
GO:0010941	0.0001334	2.87786429	8.98149027	21	456
GO:0009888	0.00015	2.7891727	9.74964404	22	495
GO:0007259	0.00018076	11.4492754	0.55149502	5	28
GO:0070486	0.00018582	5.11190878	2.06810631	9	105
GO:0010951	0.00018884	8.39302802	0.86663503	6	44
GO:0060429	0.00022955	3.17471466	6.00735643	16	305
GO:0010466	0.00024283	7.96948052	0.90602753	6	46
GO:0009892	0.00026136	2.49733267	13.0783104	26	664

GO:0071310	0.00028145	2.48350987	13.1373991	26	667
GO:0001816	0.00028679	4.35420744	2.67869008	10	136
GO:0042221	0.00029709	2.23990569	23.0249169	38	1169
GO:0002683	0.00031181	5.33333333	1.7529663	8	89
GO:0045069	0.000347	14.8896926	0.35453251	4	18
GO:0043066	0.00037569	3.2750015	5.0225439	14	255
GO:0097305	0.00039531	4.57388229	2.28476507	9	116
GO:0048584	0.00040349	2.52760417	11.1677741	23	567
GO:0009611	0.00041195	2.99564473	6.32249644	16	321
GO:0008283	0.00043936	2.55493889	10.4981016	22	533
GO:0043069	0.00044078	3.21821946	5.1013289	14	259
GO:0051716	0.00047696	2.15915367	37.6592311	53	1912
GO:0048522	0.00049614	2.15139591	25.3490745	40	1287
GO:0006955	0.0004966	2.76554828	7.76032273	18	394
GO:0031099	0.00050847	5.67284689	1.43782629	7	73
GO:0002521	0.00050858	4.40467495	2.36355007	9	120
GO:0048513	0.00053753	2.26483622	16.8599905	30	856
GO:0007155	0.00054369	2.67259383	8.50878026	19	432
GO:0022610	0.00054369	2.67259383	8.50878026	19	432
GO:0051384	0.00059051	6.62824675	1.06359753	6	54
GO:0007165	0.0006772	2.08955224	31.2579497	46	1587
GO:0097193	0.00070436	5.34342105	1.5166113	7	77
GO:0002682	0.00075678	2.65633136	8.03607024	18	408
GO:0030855	0.00077562	3.79280822	3.03322259	10	154
GO:0031960	0.00079155	6.23376623	1.12268628	6	57
GO:0030212	0.00080031	22.0928571	0.19696251	3	10
GO:0042771	0.00080031	22.0928571	0.19696251	3	10
GO:0040013	0.00082255	5.19243421	1.5560038	7	79
GO:0033993	0.00082795	3.13543599	4.80588514	13	244
GO:0048519	0.00084734	2.08944958	24.1672995	38	1227
GO:0022414	0.00086724	2.9840745	5.45586141	14	277
GO:0098609	0.00089403	3.10692826	4.84527765	13	246
GO:0060548	0.00089875	2.97200264	5.47555766	14	278
GO:0048518	0.00092869	2.04876514	29.7610346	44	1511
GO:0008630	0.00093153	10.958028	0.45301376	4	23
GO:0050777	0.00093153	10.958028	0.45301376	4	23
GO:0051249	0.00095593	5.04960882	1.5953963	7	81
GO:0097190	0.00096118	3.43315972	3.68319886	11	187
GO:0052548	0.00102873	4.98105263	1.61509255	7	82
GO:0045071	0.00108484	19.3265625	0.21665876	3	11
GO:0048701	0.00108484	19.3265625	0.21665876	3	11
GO:0019724	0.0011012	10.4075949	0.47271001	4	24
GO:0046631	0.0011012	10.4075949	0.47271001	4	24

GO:0034341	0.00112766	7.29166667	0.80754627	5	41
GO:0002523	0.00113533	101.975309	0.05908875	2	3
GO:0031340	0.00113533	101.975309	0.05908875	2	3
GO:0042574	0.00113533	101.975309	0.05908875	2	3
GO:0050665	0.00113533	101.975309	0.05908875	2	3
GO:0090280	0.00113533	101.975309	0.05908875	2	3
GO:0010605	0.0012827	2.32863822	11.3450403	22	576
GO:0051250	0.00129146	9.90958409	0.49240626	4	25
GO:0001775	0.00134238	2.95848946	5.0619364	13	257
GO:0001501	0.00139746	3.77309868	2.71808258	9	138
GO:0048608	0.00145479	4.13025641	2.20598007	8	112
GO:0052547	0.00146083	4.66398026	1.7135738	7	87
GO:0071260	0.00150358	9.45684695	0.51210252	4	26
GO:0061458	0.00154089	4.08990476	2.22567632	8	113
GO:0031324	0.00157742	2.28564773	11.5223066	22	585
GO:0045861	0.00158944	5.37794409	1.28025629	6	65
GO:0048545	0.00162581	3.68458231	2.77717133	9	141
GO:0032502	0.00170028	1.96465047	32.4397247	46	1647
GO:0006953	0.00182753	15.45375	0.25605126	3	13
GO:0030850	0.00182753	15.45375	0.25605126	3	13
GO:0070741	0.00182753	15.45375	0.25605126	3	13
GO:1903037	0.00186117	5.19906323	1.31964879	6	67
GO:0040012	0.00199721	2.94793763	4.64831514	12	236
GO:0002695	0.00199853	8.66455696	0.55149502	4	28
GO:0032269	0.00203246	2.81110491	5.29829141	13	269
GO:0048583	0.00204744	2.01744698	19.9326056	32	1012
GO:0071214	0.00216681	5.03153989	1.35904129	6	69
GO:0006925	0.0022416	50.9753086	0.078785	2	4
GO:0046597	0.0022416	50.9753086	0.078785	2	4
GO:0048245	0.0022416	50.9753086	0.078785	2	4
GO:0051770	0.0022416	50.9753086	0.078785	2	4
GO:0072606	0.0022416	50.9753086	0.078785	2	4
GO:0072677	0.0022416	50.9753086	0.078785	2	4
GO:2000643	0.0022416	50.9753086	0.078785	2	4
GO:0031100	0.00228388	8.31594937	0.57119127	4	29
GO:1903034	0.00229072	4.28130672	1.85144756	7	94
GO:0034110	0.00233317	4.95170455	1.37873754	6	70
GO:0002694	0.00243414	4.23160885	1.87114381	7	95
GO:0042127	0.00246317	2.41590528	8.173944	17	415
GO:0044767	0.00249822	1.91197535	32.0064072	45	1625
GO:0014070	0.00255605	2.73134166	5.43616516	13	276
GO:0032270	0.00259327	2.40253788	8.2133365	17	417
GO:0007166	0.00262101	2.05509554	15.9933555	27	812

GO:0044702	0.00264537	2.84045653	4.80588514	12	244
GO:0051704	0.00292162	2.22900293	10.5374941	20	535
GO:0043901	0.00293657	7.69620253	0.61058377	4	31
GO:0050789	0.00313358	2.12354068	55.3070717	67	2808
GO:0051239	0.00316723	2.06280788	14.5555292	25	739
GO:0050790	0.00323158	2.08271186	13.7676792	24	699
GO:0042110	0.00325828	3.9991511	1.96962506	7	100
GO:0070489	0.00325828	3.9991511	1.96962506	7	100
GO:0071593	0.00325828	3.9991511	1.96962506	7	100
GO:0051248	0.00328604	2.64522931	5.59373517	13	284
GO:0050663	0.00330635	7.41952984	0.63028002	4	32
GO:0009612	0.00331376	4.58723885	1.47721879	6	75
GO:0002548	0.0034289	11.8788462	0.31514001	3	16
GO:0050793	0.00353892	2.09096354	13.0586141	23	663
GO:0010604	0.00354326	2.04202586	14.6737067	25	745
GO:0001934	0.00360047	2.61423358	5.65282392	13	287
GO:0000185	0.00368824	33.9753086	0.09848125	2	5
GO:0002544	0.00368824	33.9753086	0.09848125	2	5
GO:0042730	0.00368824	33.9753086	0.09848125	2	5
GO:0060192	0.00368824	33.9753086	0.09848125	2	5
GO:0060397	0.00368824	33.9753086	0.09848125	2	5
GO:0071850	0.00368824	33.9753086	0.09848125	2	5
GO:0090026	0.00368824	33.9753086	0.09848125	2	5
GO:0090279	0.00368824	33.9753086	0.09848125	2	5
GO:2000641	0.00368824	33.9753086	0.09848125	2	5
GO:0048523	0.003692	1.90486058	22.3946369	34	1137
GO:0050866	0.00370666	7.16193802	0.64997627	4	33
GO:0050865	0.00384632	3.87129934	2.02871381	7	103
GO:1901654	0.00389658	5.34013605	1.06359753	5	54
GO:0009314	0.00409763	3.44688172	2.59990508	8	132
GO:0048704	0.00410495	11.0276786	0.33483626	3	17
GO:0050868	0.00410495	11.0276786	0.33483626	3	17
GO:0051247	0.00424387	2.2758658	8.60726151	17	437
GO:0009617	0.00428111	3.79041353	2.06810631	7	105
GO:0048856	0.00428404	1.84071206	29.9186047	42	1519
GO:0032496	0.00429744	4.33161359	1.5560038	6	79
GO:0032268	0.00445937	2.04542434	13.2949692	23	675
GO:0030198	0.00451203	3.75119617	2.08780256	7	106
GO:0043062	0.00451203	3.75119617	2.08780256	7	106
GO:0051246	0.00453551	2.01804975	14.1222117	24	717
GO:0002237	0.00457394	4.27202527	1.57570005	6	80
GO:0051607	0.00457394	4.27202527	1.57570005	6	80
GO:0031348	0.00460357	6.69661086	0.68936877	4	35

GO:0046649	0.00469913	3.36293963	2.65899383	8	135
GO:0010562	0.00479662	2.43286847	6.5391552	14	332
GO:0045937	0.00479662	2.43286847	6.5391552	14	332
GO:0046632	0.00485654	10.29	0.35453251	3	18
GO:0071479	0.00485654	10.29	0.35453251	3	18
GO:0072332	0.00485654	10.29	0.35453251	3	18
GO:1903038	0.00485654	10.29	0.35453251	3	18
GO:1903901	0.00485654	10.29	0.35453251	3	18
GO:0030334	0.00488049	2.88916563	3.88016137	10	197
GO:0042327	0.00497089	2.50616541	5.86948268	13	298
GO:0030100	0.00530986	4.93226899	1.14238253	5	58
GO:0045321	0.00533233	3.03824579	3.3089701	9	168
GO:0065007	0.0054048	2.09693878	58.4387755	69	2967
GO:0001765	0.00546174	25.4753086	0.1181775	2	6
GO:0006882	0.00546174	25.4753086	0.1181775	2	6
GO:0030214	0.00546174	25.4753086	0.1181775	2	6
GO:0042572	0.00546174	25.4753086	0.1181775	2	6
GO:0051767	0.00546174	25.4753086	0.1181775	2	6
GO:0051769	0.00546174	25.4753086	0.1181775	2	6
GO:0060396	0.00546174	25.4753086	0.1181775	2	6
GO:1900745	0.00546174	25.4753086	0.1181775	2	6
GO:0065009	0.00546341	1.92623942	16.820598	27	854
GO:0002685	0.00563634	6.287687	0.72876127	4	37
GO:1903036	0.00563634	6.287687	0.72876127	4	37
GO:0048525	0.00568596	9.64453125	0.37422876	3	19
GO:1904019	0.00568596	9.64453125	0.37422876	3	19
GO:0031325	0.00574463	1.95263814	15.2055055	25	772
GO:0050727	0.006138	4.75058275	1.18177504	5	60
GO:1903900	0.00620638	6.10126582	0.74845752	4	38
GO:0080134	0.00645577	2.27598711	7.48457523	15	380
GO:0002443	0.00658447	4.66460623	1.20147129	5	61
GO:0050670	0.00681356	5.92549729	0.76815377	4	39
GO:0042493	0.00691771	3.13333333	2.83626009	8	144
GO:0030336	0.00705329	4.58164642	1.22116754	5	62
GO:0001817	0.00737334	3.39859971	2.28476507	7	116
GO:0002449	0.0074589	5.75949367	0.78785002	4	40
GO:0032944	0.0074589	5.75949367	0.78785002	4	40
GO:1903035	0.0074589	5.75949367	0.78785002	4	40
GO:0002684	0.00748562	2.5675886	4.78618889	11	243
GO:0009636	0.00754504	4.5015473	1.24086379	5	63
GO:1902105	0.00754504	4.5015473	1.24086379	5	63
GO:0009435	0.00754897	20.3753086	0.13787375	2	7
GO:0035456	0.00754897	20.3753086	0.13787375	2	7

GO:0046596	0.00754897	20.3753086	0.13787375	2	7
GO:0055069	0.00754897	20.3753086	0.13787375	2	7
GO:0071378	0.00754897	20.3753086	0.13787375	2	7
GO:0071675	0.00754897	20.3753086	0.13787375	2	7
GO:1900744	0.00754897	20.3753086	0.13787375	2	7
GO:0030593	0.00758635	8.56875	0.41362126	3	21
GO:0034111	0.00758635	8.56875	0.41362126	3	21
GO:0034340	0.00758635	8.56875	0.41362126	3	21
GO:0050729	0.00758635	8.56875	0.41362126	3	21
GO:0060337	0.00758635	8.56875	0.41362126	3	21
GO:0071357	0.00758635	8.56875	0.41362126	3	21
GO:1990266	0.00758635	8.56875	0.41362126	3	21
GO:2000145	0.00761807	2.69246575	4.13621262	10	210
GO:0007568	0.00768736	3.80034423	1.7529663	6	89
GO:0048568	0.00771995	3.36686603	2.30446132	7	117
GO:0009893	0.00798323	1.83315527	19.0068818	29	965
GO:0045087	0.00801704	2.43619929	5.51495017	12	280
GO:0050863	0.00806025	4.42416341	1.26056004	5	64
GO:0030155	0.00831309	2.81650071	3.54532511	9	180
GO:0051259	0.00845277	3.01843972	2.93474134	8	149
GO:0022407	0.00854756	3.70909091	1.7923588	6	91
GO:0051260	0.00854756	3.70909091	1.7923588	6	91
GO:0071902	0.00854756	3.70909091	1.7923588	6	91
GO:0002698	0.00866086	8.11578947	0.43331751	3	22
GO:0008625	0.00866086	8.11578947	0.43331751	3	22
GO:0071887	0.00866086	8.11578947	0.43331751	3	22
GO:2000117	0.00866086	8.11578947	0.43331751	3	22
GO:0016192	0.00875604	2.13832045	8.48908401	16	431
GO:0002460	0.00886787	5.45369753	0.82724252	4	42
GO:0050794	0.00897492	1.85486538	52.4511153	63	2663
GO:0060627	0.00913383	2.97473193	2.97413384	8	151
GO:2000146	0.00916328	4.27700715	1.29995254	5	66
GO:0030154	0.00921041	1.77923426	21.8431419	32	1109
GO:0009628	0.00948462	2.22659105	7.07095396	14	359
GO:0050792	0.00963335	5.31256086	0.84693878	4	43
GO:0070663	0.00963335	5.31256086	0.84693878	4	43
GO:1904029	0.00963335	5.31256086	0.84693878	4	43
GO:0042325	0.0097499	2.11002132	8.58756526	16	436
GO:0007160	0.00975216	4.20698925	1.31964879	5	67
GO:0045765	0.00975216	4.20698925	1.31964879	5	67
GO:0002687	0.00982026	7.708125	0.45301376	3	23
GO:0016064	0.00982026	7.708125	0.45301376	3	23
GO:0030193	0.00982026	7.708125	0.45301376	3	23

GO:1900046	0.00982026	7.708125	0.45301376	3	23
GO:0006958	0.00993719	16.9753086	0.15757	2	8
GO:0010574	0.00993719	16.9753086	0.15757	2	8
GO:0019359	0.00993719	16.9753086	0.15757	2	8
GO:0019363	0.00993719	16.9753086	0.15757	2	8
GO:0035455	0.00993719	16.9753086	0.15757	2	8
GO:0038066	0.00993719	16.9753086	0.15757	2	8
GO:0051412	0.00993719	16.9753086	0.15757	2	8
GO:0071353	0.00993719	16.9753086	0.15757	2	8
GO:0071674	0.00993719	16.9753086	0.15757	2	8
GO:0090314	0.00993719	16.9753086	0.15757	2	8
GO:2000401	0.00993719	16.9753086	0.15757	2	8
GO:0044700	0.00996202	1.71926217	36.0441386	47	1830

Term
inflammatory response
response to stress
defense response
acute inflammatory response
single organism cell adhesion
negative regulation of molecular function
response to stimulus
cellular response to chemical stimulus
response to cytokine
negative regulation of catalytic activity
response to external stimulus
programmed cell death
cell death
death
response to external biotic stimulus
response to other organism
homotypic cell-cell adhesion
cellular response to cytokine stimulus
viral genome replication
response to biotic stimulus
regulation of apoptotic process
defense response to other organism
regulation of programmed cell death
cytokine-mediated signaling pathway
leukocyte cell-cell adhesion
response to organic substance
apoptotic process
immune system process
immune effector process
single organismal cell-cell adhesion
negative regulation of hydrolase activity
response to ionizing radiation
regulation of cell death
tissue development
JAK-STAT cascade
leukocyte aggregation
negative regulation of endopeptidase activity
epithelium development
negative regulation of peptidase activity
negative regulation of metabolic process

cellular response to organic substance
cytokine production
response to chemical
negative regulation of immune system process
regulation of viral genome replication
negative regulation of apoptotic process
response to alcohol
positive regulation of response to stimulus
response to wounding
cell proliferation
negative regulation of programmed cell death
cellular response to stimulus
positive regulation of cellular process
immune response
regeneration
leukocyte differentiation
organ development
cell adhesion
biological adhesion
response to glucocorticoid
signal transduction
intrinsic apoptotic signaling pathway
regulation of immune system process
epithelial cell differentiation
response to corticosteroid
hyaluronan metabolic process
intrinsic apoptotic signaling pathway in response to DNA damage by p53 cl
negative regulation of locomotion
response to lipid
negative regulation of biological process
reproductive process
cell-cell adhesion
negative regulation of cell death
positive regulation of biological process
intrinsic apoptotic signaling pathway in response to DNA damage
negative regulation of immune response
regulation of lymphocyte activation
apoptotic signaling pathway
regulation of endopeptidase activity
negative regulation of viral genome replication
embryonic cranial skeleton morphogenesis
B cell mediated immunity
alpha-beta T cell activation

response to interferon-gamma
leukocyte migration involved in inflammatory response
positive regulation of vesicle fusion
retinal metabolic process
hydrogen peroxide biosynthetic process
positive regulation of calcium ion import
negative regulation of macromolecule metabolic process
negative regulation of lymphocyte activation
cell activation
skeletal system development
reproductive structure development
regulation of peptidase activity
cellular response to mechanical stimulus
reproductive system development
negative regulation of cellular metabolic process
negative regulation of proteolysis
response to steroid hormone
developmental process
acute-phase response
prostate gland development
response to interleukin-6
regulation of leukocyte cell-cell adhesion
regulation of locomotion
negative regulation of leukocyte activation
negative regulation of cellular protein metabolic process
regulation of response to stimulus
cellular response to abiotic stimulus
inflammatory cell apoptotic process
negative regulation of viral entry into host cell
eosinophil chemotaxis
positive regulation of nitric-oxide synthase biosynthetic process
interleukin-8 secretion
eosinophil migration
positive regulation of early endosome to late endosome transport
organ regeneration
regulation of response to wounding
regulation of homotypic cell-cell adhesion
regulation of leukocyte activation
regulation of cell proliferation
single-organism developmental process
response to organic cyclic compound
positive regulation of cellular protein metabolic process
cell surface receptor signaling pathway

single organism reproductive process
multi-organism process
negative regulation of multi-organism process
regulation of biological process
regulation of multicellular organismal process
regulation of catalytic activity
T cell activation
T cell aggregation
lymphocyte aggregation
negative regulation of protein metabolic process
cytokine secretion
response to mechanical stimulus
monocyte chemotaxis
regulation of developmental process
positive regulation of macromolecule metabolic process
positive regulation of protein phosphorylation
activation of MAPKKK activity
chronic inflammatory response
fibrinolysis
negative regulation of lipase activity
JAK-STAT cascade involved in growth hormone signaling pathway
mitotic cell cycle arrest
positive regulation of monocyte chemotaxis
regulation of calcium ion import
regulation of early endosome to late endosome transport
negative regulation of cellular process
negative regulation of cell activation
regulation of cell activation
response to ketone
response to radiation
embryonic skeletal system morphogenesis
negative regulation of T cell activation
positive regulation of protein metabolic process
response to bacterium
anatomical structure development
response to lipopolysaccharide
regulation of cellular protein metabolic process
extracellular matrix organization
extracellular structure organization
regulation of protein metabolic process
response to molecule of bacterial origin
defense response to virus
negative regulation of defense response

lymphocyte activation
positive regulation of phosphorus metabolic process
positive regulation of phosphate metabolic process
alpha-beta T cell differentiation
cellular response to ionizing radiation
intrinsic apoptotic signaling pathway by p53 class mediator
negative regulation of leukocyte cell-cell adhesion
negative regulation of viral life cycle
regulation of cell migration
positive regulation of phosphorylation
regulation of endocytosis
leukocyte activation
biological regulation
membrane raft assembly
cellular zinc ion homeostasis
hyaluronan catabolic process
retinol metabolic process
nitric-oxide synthase biosynthetic process
regulation of nitric-oxide synthase biosynthetic process
growth hormone receptor signaling pathway
positive regulation of p38MAPK cascade
regulation of molecular function
regulation of leukocyte migration
positive regulation of response to wounding
negative regulation of viral process
epithelial cell apoptotic process
positive regulation of cellular metabolic process
regulation of inflammatory response
regulation of viral life cycle
regulation of response to stress
leukocyte mediated immunity
regulation of lymphocyte proliferation
response to drug
negative regulation of cell migration
regulation of cytokine production
lymphocyte mediated immunity
regulation of mononuclear cell proliferation
negative regulation of response to wounding
positive regulation of immune system process
response to toxic substance
regulation of leukocyte differentiation
NAD biosynthetic process
response to interferon-beta

regulation of viral entry into host cell
zinc ion homeostasis
cellular response to growth hormone stimulus
regulation of mononuclear cell migration
regulation of p38MAPK cascade
neutrophil chemotaxis
negative regulation of homotypic cell-cell adhesion
response to type I interferon
positive regulation of inflammatory response
type I interferon signaling pathway
cellular response to type I interferon
neutrophil migration
regulation of cell motility
aging
embryonic organ development
positive regulation of metabolic process
innate immune response
regulation of T cell activation
regulation of cell adhesion
protein oligomerization
regulation of cell-cell adhesion
protein homooligomerization
positive regulation of protein serine/threonine kinase activity
negative regulation of immune effector process
extrinsic apoptotic signaling pathway via death domain receptors
leukocyte apoptotic process
negative regulation of cysteine-type endopeptidase activity
vesicle-mediated transport
adaptive immune response based on somatic recombination of immune re
regulation of cellular process
regulation of vesicle-mediated transport
negative regulation of cell motility
cell differentiation
response to abiotic stimulus
regulation of viral process
regulation of leukocyte proliferation
regulation of cyclin-dependent protein kinase activity
regulation of phosphorylation
cell-matrix adhesion
regulation of angiogenesis
positive regulation of leukocyte migration
immunoglobulin mediated immune response
regulation of blood coagulation

regulation of hemostasis
complement activation, classical pathway
regulation of vascular endothelial growth factor production
nicotinamide nucleotide biosynthetic process
pyridine nucleotide biosynthetic process
response to interferon-alpha
p38MAPK cascade
response to corticosterone
cellular response to interleukin-4
mononuclear cell migration
positive regulation of protein targeting to membrane
regulation of lymphocyte migration
single organism signaling

Genes
ANO6 ANXA1 CCL2 CD44 CEBPB CHI3L1 IFI16 IL4R OSMR S100A8 SERPINA3 SERPING1 SOCS3 STAT3 TNFR
ABCC9 ANGPTL4 ANO6 ANXA1 ANXA2 C1S CCL2 CD44 CDKN1A CEBPB CHI3L1 CLIC1 COLEC12 CYP1B1 FA
ABCC9 ANO6 ANXA1 C1S CCL2 CD44 CDKN1A CEBPB CHI3L1 COLEC12 GBP3 IFI16 IFITM2 IFITM3 IL4R LGA
ANO6 CEBPB OSMR S100A8 SERPINA3 SERPING1 STAT3
ANXA1 CCL2 CD44 CEBPB CLIC1 CYP1B1 EFNA1 FAS FERMT2 IL4R LGALS3 MSN PNP S100A10 S100A8 VCL
ANGPTL4 ANXA1 ANXA2 ANXA2P2 CD44 CDKN1A CNN3 CYP1B1 DAB2 FAS GADD45A GADD45B IFI16 MV
ABCC9 ACSL5 ANGPTL4 ANO6 ANXA1 ANXA2 C1S CCL2 CD44 CDKN1A CEBPB CHI3L1 CLIC1 COLEC12 CYP1
ANO6 ANXA1 CCL2 CD44 CDKN1A CEBPB CHI3L1 COLEC12 CYP1B1 DAB2 FAS FERMT2 FSTL1 GNG5 IFITM
ANXA1 CCL2 CD44 CHI3L1 IFITM2 IFITM3 IL4R LTBR NFIL3 OSMR PLP2 SOCS3 STAT3 TIMP1 TNFRSF1A
ANGPTL4 ANXA1 ANXA2 ANXA2P2 CD44 CDKN1A CNN3 FAS GADD45A GADD45B IFI16 MVP SERPINA3 SE
ABCC9 ANO6 ANXA2 CCL2 CDKN1A CEBPB CHI3L1 EFNA1 FAS FSTL1 GADD45A GBP3 IFI16 IFITM2 IFITM3
ACSL5 ANGPTL4 ANO6 ANXA1 BNIP2 CCL2 CD44 CDKN1A CEBPB CHI3L1 CYP1B1 DAB2 FAS GADD45A GA
ACSL5 ANGPTL4 ANO6 ANXA1 BNIP2 CCL2 CD44 CDKN1A CEBPB CHI3L1 CYP1B1 DAB2 EMP1 FAS GADD4
ACSL5 ANGPTL4 ANO6 ANXA1 BNIP2 CCL2 CD44 CDKN1A CEBPB CHI3L1 CYP1B1 DAB2 EMP1 FAS GADD4
ABCC9 CCL2 CEBPB GBP3 IFI16 IFITM2 IFITM3 IL4R MAOB MGST1 S100A8 SOCS3 STOM TNFRSF1A
ABCC9 CCL2 CEBPB GBP3 IFI16 IFITM2 IFITM3 IL4R MAOB MGST1 S100A8 SOCS3 STOM TNFRSF1A
ANXA1 CCL2 CD44 CEBPB CLIC1 FAS IL4R LGALS3 PNP S100A8 VCL
CCL2 CD44 CHI3L1 IFITM2 IFITM3 IL4R LTBR NFIL3 OSMR PLP2 SOCS3 STAT3 TNFRSF1A
CCL2 IFI16 IFITM2 IFITM3 STOM
ABCC9 CCL2 CEBPB GBP3 IFI16 IFITM2 IFITM3 IL4R MAOB MGST1 S100A8 SOCS3 STOM TNFRSF1A
ACSL5 ANGPTL4 ANO6 ANXA1 BNIP2 CCL2 CD44 CDKN1A CEBPB CYP1B1 DAB2 FAS GADD45A GADD45B L
ABCC9 CEBPB GBP3 IFI16 IFITM2 IFITM3 IL4R S100A8 STOM TNFRSF1A
ACSL5 ANGPTL4 ANO6 ANXA1 BNIP2 CCL2 CD44 CDKN1A CEBPB CYP1B1 DAB2 FAS GADD45A GADD45B L
CCL2 CD44 IFITM2 IFITM3 IL4R LTBR OSMR PLP2 SOCS3 STAT3 TNFRSF1A
ANXA1 CCL2 CD44 CEBPB FAS IL4R LGALS3 MSN PNP S100A8
ANXA1 CCL2 CD44 CDKN1A CEBPB CHI3L1 COLEC12 CYP1B1 DAB2 FAS FERMT2 FSTL1 GNG5 IFITM2 IFIT
ACSL5 ANGPTL4 ANO6 ANXA1 BNIP2 CCL2 CD44 CDKN1A CEBPB CHI3L1 CYP1B1 DAB2 FAS GADD45A GA
ABCC9 ANO6 ANXA1 ANXA2 C1S CCL2 CD44 CDKN1A CEBPB COLEC12 FAS FCGR2B GBP3 IFI16 IFITM2 IFIT
ABCC9 C1S CCL2 CEBPB FAS GBP3 IFI16 IFITM2 IFITM3 IL4R LGALS3 SERPING1 STOM
ANXA1 CCL2 CD44 CEBPB CLIC1 CYP1B1 FAS IL4R LGALS3 MSN PNP S100A8 VCL
ANGPTL4 ANXA1 CD44 CNN3 FAS IFI16 SERPINA3 SERPING1 TIMP1
ANXA1 CCL2 CDKN1A GADD45A IFI16 SOCS3
ACSL5 ANGPTL4 ANO6 ANXA1 BNIP2 CCL2 CD44 CDKN1A CEBPB CYP1B1 DAB2 FAS GADD45A GADD45B L
ADAMTS9 ANO6 ANXA1 CD44 CDKN1A CEBPB CHI3L1 CNN3 CYP1B1 DAB2 EFNA1 EMP1 LGALS3 MSN PR
CCL2 CYP1B1 SOCS3 STAT3 TNFRSF1A
ANXA1 CCL2 CD44 CEBPB FAS IL4R LGALS3 PNP S100A8
CD44 FAS IFI16 SERPINA3 SERPING1 TIMP1
ADAMTS9 ANXA1 CD44 CDKN1A CEBPB CNN3 DAB2 EMP1 LGALS3 MSN RDH10 SOCS3 TAGLN2 TNC TNFR
CD44 FAS IFI16 SERPINA3 SERPING1 TIMP1
ANGPTL4 ANXA1 ANXA2 ANXA2P2 CD44 CDKN1A CEBPB CNN3 CYP1B1 DAB2 EFNA1 FAS GADD45A GAD

ANXA1 CCL2 CD44 CDKN1A CEBPB CHI3L1 COLEC12 CYP1B1 DAB2 FERMT2 FSTL1 GNG5 IFITM2 IFITM3 IL
ANXA1 CCL2 CEBPB CHI3L1 CYP1B1 IFI16 IL4R PNP S100A8 ZFP36
ANO6 ANXA1 CCL2 CD44 CDKN1A CEBPB CHI3L1 COLEC12 CYP1B1 DAB2 EFNA1 FAS FERMT2 FSTL1 GNG5
CCL2 CEBPB FAS IFI16 IL4R LGALS3 SERPING1 TMEM176A
IFI16 IFITM2 IFITM3 STOM
ANGPTL4 ANXA1 BNIP2 CCL2 CD44 CDKN1A CEBPB DAB2 FAS LGALS3 PIM1 SOCS3 STAT3 TIMP1
ANXA1 CCL2 CDKN1A MAOB MSN PIM1 S100A8 SOCS3 STAT3
ANO6 C1S CCL2 CD44 CHI3L1 COLEC12 CYP1B1 DAB2 EFNA1 FAS GADD45A GADD45B IFI16 IL4R LGALS3 L
ANO6 ANXA1 ANXA2 CCL2 CD44 CLIC1 LYVE1 MYOF OSMR S100A8 SERPING1 SOCS3 TIMP1 TNC TNFRSF1
ANXA1 ANXA2 CCL2 CDKN1A CEBPB CYP1B1 DAB2 EMP1 IFI16 IGFBP7 IL4R LGALS3 NAMPT OSMR PIM1 F
ANGPTL4 ANXA1 BNIP2 CCL2 CD44 CDKN1A CEBPB DAB2 FAS LGALS3 PIM1 SOCS3 STAT3 TIMP1
ABCC9 ACSL5 ANO6 ANXA1 ANXA2 CCL2 CD44 CDKN1A CEBPB CHI3L1 CLIC1 COLEC12 CYP1B1 DAB2 DTN
ADAMTS9 ANO6 ANXA1 ANXA2 BNIP2 CCL2 CD44 CDKN1A CEBPB CEBPD CHI3L1 CLIC1 COLEC12 CYP1B1
C1S CCL2 CD44 CDKN1A CEBPB COLEC12 FAS FCGR2B IFI16 IFITM2 IFITM3 IL4R LGALS3 NFIL3 PNP S100A
ANXA1 CCL2 CDKN1A CEBPB PRRX1 SOCS3 TNC
ANXA1 ANXA2 CEBPB FAS IFI16 IL4R LTBR PNP TMEM176A
ANO6 ANXA1 ANXA2 CCL2 CD44 CDKN1A CEBPB CHI3L1 CYP1B1 DAB2 EFNA1 FAS IFI16 IL4R LTBR MAOB
ANXA1 CCL2 CD44 CEBPB CLIC1 CYP1B1 EFNA1 FAS FERMT2 IGFBP7 IL4R LGALS3 LYVE1 MSN PNP S100A1
ANXA1 CCL2 CD44 CEBPB CLIC1 CYP1B1 EFNA1 FAS FERMT2 IGFBP7 IL4R LGALS3 LYVE1 MSN PNP S100A1
ANXA1 CCL2 CDKN1A FAS MAOB SOCS3
ABCC9 ACSL5 ANO6 ANXA1 ANXA2 CCL2 CD44 CDKN1A CEBPB CHI3L1 CLIC1 COLEC12 CYP1B1 DAB2 DTN
CD44 CDKN1A CEBPB CYP1B1 IFI16 S100A8 TNFRSF1A
ANO6 ANXA1 C1S CCL2 CDKN1A CEBPB COLEC12 FAS FCGR2B IFI16 IL4R LGALS3 MSN PNP SERPING1 SOC
ADAMTS9 ANXA1 CDKN1A CEBPB CNN3 DAB2 LGALS3 MSN TAGLN2 TNFRSF1A
ANXA1 CCL2 CDKN1A FAS MAOB SOCS3
CD44 LYVE1 PIM1
CD44 CDKN1A IFI16
CCL2 CYP1B1 IFITM2 IFITM3 STAT3 TIMP1 VCL
ANXA1 CCL2 CDKN1A CEBPB FAS IL4R MAOB MGST1 MSN PIM1 S100A8 SOCS3 STAT3
ANGPTL4 ANXA1 ANXA2 ANXA2P2 BNIP2 CCL2 CD44 CDKN1A CEBPB CNN3 CYP1B1 DAB2 EFNA1 FAS GA
ANXA1 CCL2 CD44 CEBPB IL4R LIMK2 MGST1 NAMPT PLCD1 RDH10 SOCS3 STAT3 TIMP1 TNC
ANXA1 CCL2 CD44 CEBPB CLIC1 CYP1B1 FAS IL4R LGALS3 MSN PNP S100A8 VCL
ANGPTL4 ANXA1 BNIP2 CCL2 CD44 CDKN1A CEBPB DAB2 FAS LGALS3 PIM1 SOCS3 STAT3 TIMP1
ADAMTS9 ANGPTL4 ANO6 ANXA1 ANXA2 BNIP2 C1S CCL2 CD44 CDKN1A CEBPB CEBPD CHI3L1 CLIC1 COL
CD44 CDKN1A IFI16 TNFRSF1A
IFI16 IL4R LGALS3 SERPING1
CCL2 CDKN1A CEBPB FAS IL4R LGALS3 PNP
ACSL5 CD44 CDKN1A CEBPB CYP1B1 FAS IFI16 LGALS3 LTBR S100A8 TNFRSF1A
CD44 FAS IFI16 S100A8 SERPINA3 SERPING1 TIMP1
IFI16 IFITM2 IFITM3
PRRX1 RDH10 SLC39A1
C1S FAS IL4R SERPING1
ANXA1 CEBPB IL4R PNP

CCL2 CD44 IFITM2 IFITM3 SOCS3
CCL2 S100A8
ANXA1 ANXA2
CYP1B1 RDH10
MAOB STAT3
CCL2 LGALS3
ANXA2 CD44 CDKN1A CEBPB CYP1B1 DAB2 EFNA1 FAS GADD45A GADD45B IFI16 IFITM3 MVP NFIL3 PIM
CEBPB FAS IL4R LGALS3
ANXA1 CCL2 CDKN1A CEBPB CLIC1 FAS IL4R LGALS3 LTBR PNP SERPING1 TIMP1 VCL
ANO6 ANXA2 CD44 CHI3L1 LGALS3 PRRX1 RDH10 SLC39A1 TIMP1
ANXA1 CD44 CEBPB MGST1 PLCD1 RDH10 SOCS3 TNC
CD44 FAS IFI16 S100A8 SERPINA3 SERPING1 TIMP1
FAS GADD45A LTBR TNFRSF1A
ANXA1 CD44 CEBPB MGST1 PLCD1 RDH10 SOCS3 TNC
ANXA2 CD44 CDKN1A CEBPB CYP1B1 DAB2 EFNA1 FAS GADD45A GADD45B IFI16 IFITM3 MVP NFIL3 PIM
CD44 FAS IFI16 SERPINA3 SERPING1 TIMP1
ANXA1 CCL2 CDKN1A FAS IL4R MAOB MSN SOCS3 STAT3
ADAMTS9 ANGPTL4 ANO6 ANXA1 ANXA2 BNIP2 CCL2 CD44 CDKN1A CEBPB CHI3L1 CLIC1 CNN3 CYP1B1
CEBPB SERPINA3 STAT3
ANXA1 CD44 TNC
CCL2 CHI3L1 STAT3
CCL2 CD44 CEBPB IL4R LGALS3 PNP
ANO6 CCL2 CYP1B1 DAB2 EFNA1 IFITM2 IFITM3 LGALS3 MSN STAT3 TIMP1 VCL
CEBPB FAS IL4R LGALS3
ANXA2 CD44 CDKN1A FAS GADD45A GADD45B IFI16 MVP SERPINA3 SERPING1 SOCS3 TIMP1 ZFP36
ACSL5 ANO6 ANXA2 C1S CCL2 CD44 CDKN1A CHI3L1 COLEC12 CYP1B1 DAB2 EFNA1 FAS FCGR2B GADD45
CDKN1A FAS GADD45A IFI16 LTBR TNFRSF1A
ANXA1 FAS
IFITM2 IFITM3
CCL2 LGALS3
CCL2 NAMPT
ANXA1 CHI3L1
CCL2 LGALS3
DAB2 MSN
CCL2 CDKN1A CEBPB SOCS3
ANO6 ANXA2 OSMR S100A8 SERPING1 SOCS3 TNFRSF1A
CCL2 CD44 CEBPB IL4R LGALS3 PNP
CCL2 CDKN1A CEBPB FAS IL4R LGALS3 PNP
ANXA1 ANXA2 CCL2 CDKN1A CEBPB CYP1B1 IGFBP7 IL4R LGALS3 NAMPT OSMR PLCD1 PNP PRRX1 STAT3
ADAMTS9 ANGPTL4 ANO6 ANXA1 ANXA2 BNIP2 CCL2 CD44 CDKN1A CEBPB CHI3L1 CLIC1 CNN3 CYP1B1
ANXA1 CCL2 CDKN1A COLEC12 CYP1B1 FAS IL4R MAOB MSN NAMPT PIM1 SOCS3 STAT3
ANXA2 CCL2 CD44 CDKN1A CHI3L1 DAB2 EFNA1 FAS GADD45A GADD45B IFI16 LTBR MSN PIM1 PLCE1 S1
ACSL5 ANO6 ANXA1 CCL2 CD44 CDKN1A DAB2 EFNA1 FAS FERMT2 FSTL1 IFITM2 IFITM3 IL4R LGALS3 LTB

ANXA1 CCL2 CD44 CEBPB IL4R LIMK2 MGST1 PLCD1 RDH10 SOCS3 TIMP1 TNC
ABCC9 CCL2 CEBPB FCGR2B GBP3 IFI16 IFITM2 IFITM3 IL4R LIMK2 LTBR MAOB MGST1 NAMPT S100A8 SC
IFI16 IFITM2 IFITM3 TIMP1
ABCC9 ACSL5 ADAMTS9 ANGPTL4 ANO6 ANXA1 ANXA2 ANXA2P2 BNIP2 C1S CCL2 CD44 CDKN1A CEBPB C
ADAMTS9 ANGPTL4 ANO6 ANXA1 ANXA2 CCL2 CEBPB CHI3L1 CLIC1 CYP1B1 DAB2 EFNA1 FAS IFI16 IL4R L
ANGPTL4 ANXA1 ANXA2 ANXA2P2 BNIP2 CCL2 CD44 CDKN1A CHI3L1 CNN3 EFNA1 FAS GADD45A GADD4
ANXA1 CCL2 CEBPB FAS IL4R LGALS3 PNP
ANXA1 CCL2 CEBPB FAS IL4R LGALS3 PNP
ANXA1 CCL2 CEBPB FAS IL4R LGALS3 PNP
ANXA2 CD44 CDKN1A FAS GADD45A GADD45B IFI16 MVP SERPINA3 SERPING1 SOCS3 TIMP1 ZFP36
ANXA1 CHI3L1 IL4R PNP
CCL2 CHI3L1 FAS GADD45A LTBR TNFRSF1A
ANO6 CCL2 LGALS3
ADAMTS9 ANGPTL4 ANO6 BNIP2 CCL2 CEBPB CHI3L1 CLIC1 CYP1B1 DAB2 EFNA1 FAS FERMT2 IL4R MSN I
ANXA2 CCL2 CD44 CDKN1A CEBPB CEBPD CHI3L1 DAB2 EFNA1 FAS GADD45A GADD45B IFI16 LTBR MSN I
ANXA2 CCL2 CD44 CDKN1A CHI3L1 DAB2 EFNA1 GADD45A GADD45B LTBR PIM1 PLCE1 TNFRSF1A
GADD45A GADD45B
CEBPB S100A8
ANXA2 SERPING1
ANGPTL4 ANXA1
SOCS3 STAT3
CDKN1A GADD45A
ANO6 CCL2
CCL2 LGALS3
DAB2 MSN
ANGPTL4 ANXA1 ANXA2 BNIP2 CCL2 CD44 CDKN1A CEBPB CYP1B1 DAB2 EFNA1 FAS GADD45A GADD45B
CEBPB FAS IL4R LGALS3
CCL2 CDKN1A CEBPB FAS IL4R LGALS3 PNP
CCL2 CDKN1A MAOB MSN SOCS3
ANXA1 CCL2 CDKN1A GADD45A IFI16 RDH10 SCARA3 SOCS3
PRRX1 RDH10 SLC39A1
CEBPB IL4R LGALS3
ANXA2 CCL2 CD44 CDKN1A CHI3L1 DAB2 EFNA1 FAS GADD45A GADD45B IFI16 LTBR MSN PIM1 PLCE1 S1
CCL2 CEBPB MAOB MGST1 S100A8 SOCS3 TNFRSF1A
ADAMTS9 ANGPTL4 ANO6 ANXA1 ANXA2 BNIP2 CCL2 CD44 CDKN1A CEBPB CHI3L1 CNN3 CYP1B1 DAB2 E
CCL2 CEBPB MAOB MGST1 S100A8 SOCS3
ANXA2 CCL2 CD44 CDKN1A CHI3L1 DAB2 EFNA1 FAS GADD45A GADD45B IFI16 LTBR MSN MVP PIM1 PLC
ANXA2 CD44 CYP1B1 LGALS3 LTBP1 TIMP1 TNC
ANXA2 CD44 CYP1B1 LGALS3 LTBP1 TIMP1 TNC
ANXA2 CCL2 CD44 CDKN1A CEBPB CHI3L1 DAB2 EFNA1 FAS GADD45A GADD45B IFI16 LTBR MSN MVP PII
CCL2 CEBPB MAOB MGST1 S100A8 SOCS3
ABCC9 GBP3 IFI16 IFITM2 IFITM3 STOM
IFI16 SERPING1 SOCS3 TNFRSF1A

ANXA1 CCL2 CDKN1A CEBPB FAS IL4R LGALS3 PNP
ANXA2 CCL2 CD44 CDKN1A CHI3L1 DAB2 EFNA1 GADD45A GADD45B LTBR PIM1 PLCE1 STAT3 TNFRSF1A
ANXA2 CCL2 CD44 CDKN1A CHI3L1 DAB2 EFNA1 GADD45A GADD45B LTBR PIM1 PLCE1 STAT3 TNFRSF1A
ANXA1 IL4R PNP
CDKN1A GADD45A IFI16
CD44 CDKN1A IFI16
CEBPB IL4R LGALS3
IFI16 IFITM2 IFITM3
ANO6 CCL2 CYP1B1 DAB2 EFNA1 LGALS3 MSN STAT3 TIMP1 VCL
ANXA2 CCL2 CD44 CDKN1A CHI3L1 DAB2 EFNA1 GADD45A GADD45B LTBR PIM1 PLCE1 TNFRSF1A
ANO6 ANXA2 CCL2 DAB2 LGALS3
ANXA1 CCL2 CDKN1A CEBPB FAS IL4R LGALS3 LTBR PNP
ABCC9 ACSL5 ADAMTS9 ANGPTL4 ANO6 ANXA1 ANXA2 ANXA2P2 BNIP2 C1S CCL2 CD44 CDKN1A CEBPB
ANXA2 S100A10
S100A8 SLC39A14
CD44 LYVE1
CYP1B1 RDH10
CCL2 NAMPT
CCL2 NAMPT
SOCS3 STAT3
GADD45A GADD45B
ANGPTL4 ANXA1 ANXA2 ANXA2P2 BNIP2 CCL2 CD44 CDKN1A CHI3L1 CNN3 CYP1B1 DAB2 EFNA1 FAS GA
ANO6 CCL2 LGALS3 MSN
ANO6 OSMR S100A8 TNFRSF1A
IFI16 IFITM2 IFITM3
ANGPTL4 ANO6 FAS
ANXA1 ANXA2 CCL2 CD44 CDKN1A CEBPB CEBPD CHI3L1 DAB2 EFNA1 FAS GADD45A GADD45B IFI16 LTB
OSMR S100A8 SERPING1 SOCS3 TNFRSF1A
IFI16 IFITM2 IFITM3 STOM
ANO6 ANXA2 CD44 COLEC12 GADD45A GADD45B IFI16 LTBR OSMR PRRX1 S100A8 SERPING1 SOCS3 STO
C1S CCL2 FAS IL4R SERPING1
CDKN1A CEBPB LGALS3 PNP
ANXA1 CCL2 CDKN1A MAOB MGST1 PNP SOCS3 STAT3
CCL2 CYP1B1 STAT3 TIMP1 VCL
ANXA1 CCL2 CEBPB CYP1B1 IFI16 IL4R ZFP36
C1S FAS IL4R SERPING1
CDKN1A CEBPB LGALS3 PNP
ANXA2 SERPING1 SOCS3 TNFRSF1A
ANO6 ANXA1 C1S CCL2 CDKN1A COLEC12 IFI16 IL4R LGALS3 PNP SERPING1
CCL2 CDKN1A CYP1B1 FAS MAOB
CEBPB FAS IL4R PNP TMEM176A
NAMPT PNP
IFITM2 IFITM3

IFITM2 IFITM3
S100A8 SLC39A14
SOCS3 STAT3
CCL2 LGALS3
GADD45A GADD45B
CCL2 LGALS3 S100A8
CEBPB IL4R LGALS3
IFITM2 IFITM3 SOCS3
OSMR S100A8 TNFRSF1A
IFITM2 IFITM3 SOCS3
IFITM2 IFITM3 SOCS3
CCL2 LGALS3 S100A8
ANO6 CCL2 CYP1B1 DAB2 EFNA1 LGALS3 MSN STAT3 TIMP1 VCL
CCL2 CDKN1A SERPING1 SOCS3 STAT3 TIMP1
CEBPB EFNA1 PLCD1 PRRX1 RDH10 SLC39A1 SOCS3
ANXA1 ANXA2 BNIP2 CCL2 CD44 CDKN1A CEBPB CEBPD CHI3L1 DAB2 EFNA1 FAS GADD45A GADD45B IFI
C1S CCL2 CD44 CDKN1A COLEC12 IFI16 IFITM2 IFITM3 LGALS3 S100A8 SERPING1 SOCS3
CCL2 CEBPB IL4R LGALS3 PNP
CCL2 CD44 CEBPB CYP1B1 EFNA1 IL4R LGALS3 PNP S100A10
ANGPTL4 ANXA2 ATL3 COLEC12 FAS MGST1 S100A10 STOM
CCL2 CD44 CEBPB IL4R LGALS3 PNP
ANGPTL4 ATL3 COLEC12 FAS MGST1 STOM
CHI3L1 EFNA1 GADD45A GADD45B PIM1 PLCE1
IL4R LGALS3 SERPING1
FAS LGALS3 TNFRSF1A
ANXA1 FAS LGALS3
CD44 FAS IFI16
ADAMTS9 ANO6 ANXA1 ANXA2 CCL2 COLEC12 DAB2 IL4R LGALS3 MARCH3 MSN S100A10 SCARA3 SERPI
C1S FAS IL4R SERPING1
ABCC9 ACSL5 ADAMTS9 ANGPTL4 ANO6 ANXA1 ANXA2 BNIP2 CCL2 CD44 CDKN1A CEBPB CEBPD CHI3L1
ANO6 ANXA1 ANXA2 CCL2 DAB2 IL4R LGALS3 MSN
CCL2 CYP1B1 STAT3 TIMP1 VCL
ADAMTS9 ANGPTL4 ANXA1 ANXA2 BNIP2 CCL2 CDKN1A CEBPB CLIC1 CNN3 DAB2 EFNA1 FAS FERMT2 GA
ANGPTL4 ANXA1 CCL2 CDKN1A CHI3L1 FAS GADD45A IFI16 LTBR MYOF RDH10 SCARA3 SOCS3 TNFRSF1A
IFI16 IFITM2 IFITM3 STOM
CDKN1A CEBPB LGALS3 PNP
CDKN1A GADD45A PIM1 SOCS3
ANXA2 CCL2 CD44 CDKN1A CHI3L1 DAB2 EFNA1 GADD45A GADD45B LTBR MVP PIM1 PLCE1 SOCS3 STAT
CD44 FERMT2 LYVE1 S100A10 VCL
ANGPTL4 CCL2 CHI3L1 CYP1B1 EFNA1
ANO6 CCL2 LGALS3
C1S IL4R SERPING1
ANO6 ANXA2 SERPING1

ANO6 ANXA2 SERPING1
C1S SERPING1
CCL2 CYP1B1
NAMPT PNP
NAMPT PNP
IFITM2 IFITM3
GADD45A GADD45B
CDKN1A MAOB
IL4R NFIL3
CCL2 LGALS3
CCL2 STOM
CCL2 MSN
ABCC9 ACSL5 ANO6 ANXA1 ANXA2 CCL2 CD44 CDKN1A CEBPB CHI3L1 CLIC1 COLEC12 CYP1B1 DAB2 DTN

padjust
6.89E-05
0.00023397
0.00081985
0.00081985
0.0016417
0.00192541
0.00192554
0.00254928
0.00254928
0.00322413
0.00568682
0.00568682
0.00568682
0.00568682
0.00568682
0.00568682
0.00568682
0.00568682
0.00568682
0.00568682
0.00568682
0.00568682
0.00617593
0.00634125
0.00681185
0.00815249
0.00844705
0.00844705
0.00844705
0.00844705
0.00844705
0.010273
0.01053867
0.01150114
0.01330582
0.01330582
0.01330582
0.01574825
0.01623203
0.01703408

0.01780153
0.01780153
0.01801177
0.01847456
0.02010302
0.02129176
0.02191452
0.02191452
0.02191733
0.02253182
0.02253182
0.02367634
0.02367634
0.02367634
0.02367634
0.02367634
0.02402376
0.02402376
0.02402376
0.02565747
0.02894205
0.02961726
0.03114049
0.03114049
0.03114049
0.03114049
0.03114049
0.03128214
0.03128214
0.03155753
0.03184369
0.03195397
0.03195397
0.03195397
0.03195397
0.03195397
0.03212567
0.03212567
0.03325633
0.03325633
0.03325633
0.03325633
0.03325633

0.03325633
0.03325633
0.03325633
0.03325633
0.03325633
0.03325633
0.03699818
0.03699818
0.03803892
0.03917389
0.04008833
0.04008833
0.04083164
0.04141336
0.04185525
0.04185525
0.04238486
0.0438873
0.04581134
0.04581134
0.04581134
0.04621016
0.04869316
0.04869316
0.04896949
0.04896949
0.04994739
0.04994739
0.04994739
0.04994739
0.04994739
0.04994739
0.04994739
0.04994739
0.05018405
0.05018405
0.05068814
0.05244473
0.05263507
0.05295004
0.05373893
0.05408521
0.05422995

0.054303
0.0593461
0.0593461
0.06260128
0.06260128
0.06260128
0.06260128
0.06260128
0.06260128
0.06260128
0.06260128
0.06260128
0.06315864
0.06315864
0.06315864
0.06315864
0.06315864
0.06315864
0.06315864
0.06315864
0.06315864
0.06315864
0.06315864
0.06315864
0.06315864
0.06315864
0.06315864
0.06511276
0.06553793
0.06773167
0.06773167
0.06773167
0.06915693
0.06915693
0.06915693
0.06915693
0.07097774
0.07097774
0.07097774
0.07097774
0.07097774
0.07097774
0.07101491

0.07148003
0.07148003
0.07148003
0.07148003
0.07148003
0.07148003
0.07148003
0.07148003
0.07148003
0.07239732
0.07457125
0.07457125
0.07457125
0.07457125
0.07457125
0.07457125
0.07457125
0.07457125
0.07457125
0.07457125
0.07457125
0.07457125
0.07601686
0.07601686
0.07601686
0.07601686
0.07640946
0.08122724
0.08171728
0.08457379
0.08582855
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806

0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08826806
0.08866034
0.08866034
0.09126821
0.09126821
0.09136124
0.09381917
0.09447222
0.09447222
0.09447222
0.09447222
0.09447222
0.09447222
0.09447222
0.09447222
0.09511251
0.09592758
0.09668432
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668

0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668
0.09690668

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0007268	1.64E-13	2.59356562	56.1877076	109	385
GO:0007267	1.52E-10	2.12960509	74.4304699	125	510
GO:0050803	6.81E-10	3.56376518	17.950878	45	123
GO:0051648	3.24E-09	3.90815535	13.8644993	37	95
GO:1902578	3.97E-09	1.69665088	190.162553	253	1303
GO:0044765	5.63E-09	1.69519808	182.427622	244	1250
GO:0006810	9.40E-09	1.66200846	206.65401	269	1416
GO:0051650	1.80E-08	3.74984876	13.426673	35	92
GO:0065008	2.16E-08	1.68270985	162.725439	220	1115
GO:0030001	2.55E-08	2.21236029	46.1177029	82	316
GO:0051049	3.78E-08	1.86028213	86.543664	132	593
GO:0031175	4.79E-08	1.97687113	65.5280019	106	449
GO:0048812	5.79E-08	2.1008342	51.5175605	88	353
GO:0048666	6.28E-08	1.92379553	71.5116279	113	490
GO:0051234	8.24E-08	1.60387652	210.740389	269	1444
GO:0032990	8.98E-08	1.98288117	61.4416232	100	421
GO:0097479	9.49E-08	4.30303437	9.48623636	27	65
GO:0034220	1.03E-07	2.02527946	56.0417655	93	384
GO:0044708	1.12E-07	2.53964552	27.5830565	55	189
GO:0098660	1.92E-07	2.20641279	39.6962506	71	272
GO:0048858	2.17E-07	1.94903076	60.8578548	98	417
GO:0007409	2.25E-07	2.13462898	43.6366872	76	299
GO:0048489	2.81E-07	4.13662765	9.34029426	26	64
GO:0097480	2.81E-07	4.13662765	9.34029426	26	64
GO:0048667	3.57E-07	2.04334554	48.7446607	82	334
GO:0051130	3.57E-07	2.04334554	48.7446607	82	334
GO:0007399	6.01E-07	1.63724392	130.618178	178	895
GO:0051656	6.33E-07	2.86822289	17.8049359	39	122
GO:0006811	7.38E-07	1.76278106	83.9167062	124	575
GO:0055085	7.92E-07	1.81216422	73.116991	111	501
GO:0050877	1.21E-06	1.99152173	47.723066	79	327
GO:0050808	1.32E-06	2.95605843	15.6158045	35	107
GO:0023061	1.44E-06	2.3750403	26.7074039	51	183
GO:0098662	1.81E-06	2.1547636	35.0261035	62	240
GO:0061564	1.84E-06	1.99120687	45.8258187	76	314
GO:0051179	2.56E-06	1.4975247	252.771713	305	1732
GO:0015988	3.15E-06	10.9059051	2.48101566	11	17
GO:0015991	3.15E-06	10.9059051	2.48101566	11	17
GO:0050890	3.77E-06	2.61011905	18.9724727	39	130
GO:0010975	3.91E-06	2.4134349	23.2047935	45	159

GO:0016079	3.93E-06	4.55744966	6.4214523	19	44
GO:0098655	3.95E-06	2.05190167	38.0908875	65	261
GO:0051640	4.49E-06	2.45336906	21.8913147	43	150
GO:0030030	4.73E-06	1.69611149	82.4572852	119	565
GO:0007611	5.42E-06	2.72402741	16.491457	35	113
GO:0007626	5.69E-06	2.93196169	13.8644993	31	95
GO:0060341	6.05E-06	1.84378276	54.4364025	85	373
GO:0006836	6.22E-06	2.74965003	15.9076887	34	109
GO:0050807	6.25E-06	4.13793103	7.15116279	20	49
GO:0007269	6.38E-06	2.97435897	13.2807309	30	91
GO:0000904	7.43E-06	1.81856187	56.3336497	87	386
GO:0009161	9.19E-06	2.96928328	12.8429046	29	88
GO:0051963	9.48E-06	5.03294965	5.10797342	16	35
GO:0006812	9.65E-06	1.79697635	57.5011865	88	394
GO:0043269	1.11E-05	2.02970003	35.3179877	60	242
GO:0051649	1.15E-05	1.57278744	113.688894	153	779
GO:0051641	1.17E-05	1.54268316	129.888467	171	890
GO:0007610	1.30E-05	1.92801436	41.73944	68	286
GO:0010976	1.33E-05	2.83253205	13.7185572	30	94
GO:0031344	1.48E-05	2.13862577	28.7505933	51	197
GO:0009167	2.17E-05	2.86201022	12.6969625	28	87
GO:0051962	2.23E-05	2.21243633	24.6642145	45	169
GO:0048167	2.44E-05	2.90515671	12.1131941	27	83
GO:0030182	2.53E-05	1.62340792	83.4788799	117	572
GO:0034765	2.62E-05	2.19410526	24.8101566	45	170
GO:0009126	2.75E-05	2.81351505	12.8429046	28	88
GO:0009123	3.03E-05	2.73344177	13.5726151	29	93
GO:0001505	3.74E-05	2.54437122	15.7617466	32	108
GO:0034762	4.91E-05	2.12362301	25.393925	45	174
GO:0051965	5.43E-05	5.15968992	4.08637874	13	28
GO:0042391	5.71E-05	2.10668016	25.5398671	45	175
GO:0032989	6.64E-05	1.60022586	78.2249644	109	536
GO:0044763	7.26E-05	1.57159513	491.678927	526	3369
GO:0046034	7.29E-05	2.88243655	10.7997152	24	74
GO:0032879	7.47E-05	1.50395516	113.834836	149	780
GO:0015672	7.99E-05	1.89589177	35.1720456	57	241
GO:0044699	8.78E-05	1.70862582	530.061699	559	3632
GO:0051960	9.15E-05	1.80641711	41.73944	65	286
GO:0006887	9.82E-05	2.12576313	23.0588514	41	158
GO:0000902	0.00010655	1.58823529	75.5980066	105	518
GO:1902108	0.00012409	7.62093352	2.33507356	9	16
GO:0048699	0.00012531	1.53594242	89.9003322	121	616
GO:0046128	0.00014021	2.3651812	16.0536308	31	110

GO:0060359	0.00014307	3.67073327	6.12956811	16	42
GO:0055082	0.00014468	1.9272992	30.3559563	50	208
GO:0009119	0.00016825	2.33495291	16.1995729	31	111
GO:0042278	0.00016825	2.33495291	16.1995729	31	111
GO:0045666	0.00017046	2.29682267	16.9292833	32	116
GO:0009141	0.00017098	2.56027165	12.6969625	26	87
GO:0007411	0.00017186	1.86096257	33.7126246	54	231
GO:0097485	0.00017186	1.86096257	33.7126246	54	231
GO:0061024	0.00017707	1.69327076	50.0581395	74	343
GO:0032940	0.00017843	1.71153403	47.5771239	71	326
GO:0003008	0.00018577	1.56472466	74.8682962	103	513
GO:0036465	0.00018856	5.9322314	2.91884196	10	20
GO:1903530	0.00019566	1.91069811	29.91813	49	205
GO:0007006	0.0002037	3.96894065	5.10797342	14	35
GO:0009259	0.00020617	2.03571429	23.7885619	41	163
GO:0009199	0.00022931	2.61670512	11.5294257	24	79
GO:0009205	0.00022931	2.61670512	11.5294257	24	79
GO:0008104	0.00024144	1.4748454	104.640484	136	717
GO:0097345	0.00026176	7.89236683	2.04318937	8	14
GO:1902110	0.00026176	7.89236683	2.04318937	8	14
GO:1902686	0.00026176	7.89236683	2.04318937	8	14
GO:0007612	0.00027639	2.79214366	9.63217845	21	66
GO:1902600	0.00028269	3.574	5.83768391	15	40
GO:0046903	0.0002977	1.64584912	52.5391552	76	360
GO:0019725	0.00030628	1.78748513	36.0476981	56	247
GO:0016192	0.00032448	1.58512068	62.9010441	88	431
GO:1904062	0.00034882	2.52346603	11.8213099	24	81
GO:0019693	0.00035958	1.96882086	24.3723303	41	167
GO:0051046	0.00036491	1.82393617	32.2532036	51	221
GO:0009150	0.00037346	1.9826087	23.6426198	40	162
GO:0006839	0.00039464	2.30398357	14.7401519	28	101
GO:0007416	0.0003979	2.77975376	9.19435216	20	63
GO:1902580	0.00040042	1.58822918	59.8362601	84	410
GO:0009144	0.00042692	2.47925783	11.967252	24	82
GO:0030534	0.00047032	2.58096088	10.6537731	22	73
GO:0035794	0.00048972	6.76300306	2.18913147	8	15
GO:0035418	0.00055341	8.27565789	1.75130517	7	12
GO:0006163	0.00060808	1.90604396	24.9560987	41	171
GO:0022008	0.00062574	1.45686852	93.2570005	121	639
GO:0009116	0.00064308	2.11785881	17.3671096	31	119
GO:0031346	0.00064308	2.11785881	17.3671096	31	119
GO:0006813	0.00065629	2.29217018	13.7185572	26	94
GO:0017157	0.00071046	2.48216615	10.9456573	22	75

GO:0010256	0.00074467	1.86641515	25.9776934	42	178
GO:0008637	0.00075293	3.33018303	5.69174181	14	39
GO:0006873	0.00078208	1.87608225	25.2479829	41	173
GO:0017156	0.00079848	3.51109937	5.10797342	13	35
GO:0050804	0.00082339	1.93934106	22.1831989	37	152
GO:0015992	0.00082567	2.75222265	8.31869957	18	57
GO:1901657	0.00085085	2.04664063	18.3887043	32	126
GO:0045664	0.00085392	1.77313202	30.9397247	48	212
GO:0007214	0.00085534	5.91598023	2.33507356	8	16
GO:0010959	0.00092263	1.98626406	19.9940674	34	137
GO:0030003	0.00092922	1.87125042	24.6642145	40	169
GO:0033036	0.00095827	1.39611699	117.921215	147	808
GO:0050770	0.00096402	2.54031825	9.77812055	20	67
GO:0006818	0.00103817	2.68266332	8.46464167	18	58
GO:0015682	0.00105277	4.84428443	2.91884196	9	20
GO:0072512	0.00105277	4.84428443	2.91884196	9	20
GO:0060052	0.00106047	14.7418033	1.02159468	5	7
GO:0007005	0.00106178	1.75074903	31.2316089	48	214
GO:0007613	0.00106385	2.88642687	7.15116279	16	49
GO:0055080	0.00107444	1.7968003	28.0208828	44	192
GO:0071804	0.00107619	2.33108108	11.967252	23	82
GO:0071805	0.00107619	2.33108108	11.967252	23	82
GO:0046907	0.00108579	1.46921305	77.4952539	102	531
GO:0070585	0.00118363	2.48669468	9.92406265	20	68
GO:0006753	0.0012344	1.7249055	32.2532036	49	221
GO:0008543	0.00125848	2.09821124	15.7617466	28	108
GO:1902582	0.00139961	1.48420637	68.3009018	91	468
GO:0006091	0.00140745	1.83605957	24.3723303	39	167
GO:0035773	0.00141136	5.2571847	2.48101566	8	17
GO:0048488	0.00141136	5.2571847	2.48101566	8	17
GO:0061178	0.00141136	5.2571847	2.48101566	8	17
GO:0006816	0.00149828	1.96086393	18.9724727	32	130
GO:0042220	0.00160727	4.43935644	3.06478405	9	21
GO:0046902	0.00160727	4.43935644	3.06478405	9	21
GO:0070838	0.00163516	1.86689298	22.1831989	36	152
GO:0044344	0.00165581	2.02152949	16.7833412	29	115
GO:0072655	0.00169072	2.46232127	9.48623636	19	65
GO:0015031	0.00184147	1.43867678	78.6627907	102	539
GO:0010769	0.0018478	1.9768949	17.6589938	30	121
GO:0072511	0.00184933	1.85040521	22.329141	36	153
GO:0035725	0.0018623	2.5949747	8.17275748	17	56
GO:0016043	0.00188243	1.29480584	254.668961	288	1745
GO:0008286	0.00191064	1.99772469	16.9292833	29	116

GO:0030705	0.00192362	3.08717608	5.54579972	13	38
GO:0006996	0.00195454	1.34289588	139.374703	168	955
GO:0071840	0.00196226	1.29285919	258.755339	292	1773
GO:0045184	0.00197464	1.42163233	84.2085904	108	577
GO:0098771	0.00207136	1.72379284	28.8965354	44	198
GO:0006875	0.00208743	1.83419689	22.4750831	36	154
GO:0010970	0.00210896	3.23563998	4.96203132	12	34
GO:0048588	0.00214964	2.27805326	11.0915994	21	76
GO:0007270	0.00216334	2.22596965	11.8213099	22	81
GO:0051259	0.00219593	1.84475197	21.7453726	35	149
GO:0071774	0.00219853	1.97446091	17.0752254	29	117
GO:0090382	0.00221989	4.73014827	2.62695776	8	18
GO:1902803	0.00221989	4.73014827	2.62695776	8	18
GO:0009117	0.00232909	1.67941078	31.5234931	47	216
GO:0090559	0.00237355	4.09672506	3.21072615	9	22
GO:0072521	0.00248399	1.7389336	26.7074039	41	183
GO:0001844	0.00248897	9.82513661	1.16753678	5	8
GO:0048148	0.00248897	9.82513661	1.16753678	5	8
GO:1901030	0.00248897	9.82513661	1.16753678	5	8
GO:0060627	0.00278971	1.81190547	22.0372568	35	151
GO:2001257	0.00279269	3.09409474	5.10797342	12	35
GO:1990138	0.00293258	2.38123953	9.19435216	18	63
GO:0006796	0.00297033	1.329225	134.99644	162	925
GO:0050767	0.00301008	1.60273132	36.9233507	53	253
GO:0051128	0.00309367	1.37706521	95.3001898	119	653
GO:0007340	0.00309549	Inf	0.43782629	3	3
GO:0033693	0.00309549	Inf	0.43782629	3	3
GO:0043968	0.00309549	Inf	0.43782629	3	3
GO:0045110	0.00309549	Inf	0.43782629	3	3
GO:1903937	0.00309549	Inf	0.43782629	3	3
GO:0007169	0.00321506	1.52964545	46.4095871	64	318
GO:0032410	0.00335154	4.29893665	2.77289986	8	19
GO:0033572	0.00335154	4.29893665	2.77289986	8	19
GO:0032409	0.00340902	2.04728064	13.7185572	24	94
GO:0006793	0.0035453	1.3186888	138.353109	165	948
GO:1901698	0.00356302	1.49797881	50.9337921	69	349
GO:0044802	0.00359711	1.54716746	42.3232084	59	290
GO:0055086	0.00360835	1.61601885	33.8585667	49	232
GO:0050801	0.00376329	1.62877408	32.2532036	47	221
GO:0006536	0.00397362	5.8998358	1.75130517	6	12
GO:0051205	0.00397362	5.8998358	1.75130517	6	12
GO:0050806	0.00404674	2.43825179	8.02681538	16	55
GO:0022607	0.00405908	1.35231339	102.451353	126	702

GO:0032869	0.00414011	1.80873167	20.1400095	32	138
GO:0015980	0.0043627	1.81988652	19.410299	31	133
GO:0048278	0.00445068	3.28833792	4.08637874	10	28
GO:0050772	0.00445068	3.28833792	4.08637874	10	28
GO:0010822	0.00447918	2.59660982	6.7133365	14	46
GO:0009914	0.00466452	1.89831933	16.345515	27	112
GO:0006120	0.00469444	4.59247076	2.33507356	7	16
GO:0031345	0.00492052	2.37662771	8.17275748	16	56
GO:0051204	0.00493161	7.36680328	1.31347888	5	9
GO:0050769	0.00493524	1.76532585	21.1616042	33	145
GO:0055065	0.00504112	1.68986456	25.2479829	38	173
GO:0010243	0.00508949	1.48686106	48.1608923	65	330
GO:0034776	0.00527582	11.7741408	0.87565259	4	6
GO:0051531	0.00527582	11.7741408	0.87565259	4	6
GO:0051532	0.00527582	11.7741408	0.87565259	4	6
GO:0071420	0.00527582	11.7741408	0.87565259	4	6
GO:1903421	0.00527582	11.7741408	0.87565259	4	6
GO:0046883	0.0054377	1.98761261	13.426673	23	92
GO:0019722	0.00597738	2.7347876	5.54579972	12	38
GO:0010770	0.00601185	2.24518766	9.04841006	17	62
GO:0032868	0.00645426	1.71133514	22.329141	34	153
GO:0007173	0.0064784	1.81830975	17.5130517	28	120
GO:0048878	0.00674442	1.48137677	45.2420503	61	310
GO:0019637	0.00675733	1.45106471	51.3716184	68	352
GO:0038127	0.00691505	1.78667183	18.3887043	29	126
GO:0050773	0.00702183	2.34276316	7.73493118	15	53
GO:0061025	0.00702183	2.34276316	7.73493118	15	53
GO:0046879	0.00716301	1.84715822	16.0536308	26	110
GO:1901699	0.00782698	1.53620988	35.1720456	49	241
GO:0007156	0.00799129	2.48547851	6.4214523	13	44
GO:0008344	0.00799129	2.48547851	6.4214523	13	44
GO:0035637	0.00845164	2.28205128	7.88087328	15	54
GO:0048468	0.00855438	1.30835723	107.413384	129	736
GO:0016358	0.00856435	1.92644579	13.1347888	22	90
GO:0017158	0.00866869	3.12929528	3.79449454	9	26
GO:1901379	0.00866869	3.12929528	3.79449454	9	26
GO:0022604	0.00867658	1.59953623	27.7289986	40	190
GO:0014046	0.00869054	5.89180328	1.45942098	5	10
GO:0014059	0.00869054	5.89180328	1.45942098	5	10
GO:0044085	0.00880701	1.30566254	108.434979	130	743
GO:0070201	0.00899078	1.53575666	33.7126246	47	231
GO:0048011	0.00900147	1.69328618	21.1616042	32	145
GO:0006461	0.00911527	1.40642836	57.3552444	74	393

GO:0070271	0.00911527	1.40642836	57.3552444	74	393
GO:0051050	0.00946209	1.49171018	38.9665401	53	267
GO:0051924	0.00950149	2.01692833	10.9456573	19	75
GO:0010720	0.00967002	1.61763443	25.393925	37	174
GO:0032386	0.00967002	1.61763443	25.393925	37	174
GO:0050905	0.00978163	2.40713248	6.5673944	13	45
GO:0030073	0.00979462	1.89798861	13.2807309	22	91
GO:0019228	0.00996326	4.42241379	2.04318937	6	14
GO:0010638	0.00997933	1.67795131	21.3075463	32	146
GO:0022406	0.00998945	2.81621409	4.52420503	10	31

Term
synaptic transmission
cell-cell signaling
regulation of synapse structure or activity
vesicle localization
single-organism localization
single-organism transport
transport
establishment of vesicle localization
regulation of biological quality
metal ion transport
regulation of transport
neuron projection development
neuron projection morphogenesis
neuron development
establishment of localization
cell part morphogenesis
synaptic vesicle localization
ion transmembrane transport
single-organism behavior
inorganic ion transmembrane transport
cell projection morphogenesis
axonogenesis
synaptic vesicle transport
establishment of synaptic vesicle localization
cell morphogenesis involved in neuron differentiation
positive regulation of cellular component organization
nervous system development
establishment of organelle localization
ion transport
transmembrane transport
neurological system process
synapse organization
signal release
inorganic cation transmembrane transport
axon development
localization
energy coupled proton transmembrane transport, against electrochemical
ATP hydrolysis coupled proton transport
cognition
regulation of neuron projection development

synaptic vesicle exocytosis
cation transmembrane transport
organelle localization
cell projection organization
learning or memory
locomotory behavior
regulation of cellular localization
neurotransmitter transport
regulation of synapse organization
neurotransmitter secretion
cell morphogenesis involved in differentiation
ribonucleoside monophosphate metabolic process
regulation of synapse assembly
cation transport
regulation of ion transport
establishment of localization in cell
cellular localization
behavior
positive regulation of neuron projection development
regulation of cell projection organization
purine ribonucleoside monophosphate metabolic process
positive regulation of nervous system development
regulation of synaptic plasticity
neuron differentiation
regulation of ion transmembrane transport
purine nucleoside monophosphate metabolic process
nucleoside monophosphate metabolic process
regulation of neurotransmitter levels
regulation of transmembrane transport
positive regulation of synapse assembly
regulation of membrane potential
cellular component morphogenesis
single-organism cellular process
ATP metabolic process
regulation of localization
monovalent inorganic cation transport
single-organism process
regulation of nervous system development
exocytosis
cell morphogenesis
regulation of mitochondrial membrane permeability involved in apoptotic
generation of neurons
purine ribonucleoside metabolic process

response to ammonium ion
cellular chemical homeostasis
ribonucleoside metabolic process
purine nucleoside metabolic process
positive regulation of neuron differentiation
nucleoside triphosphate metabolic process
axon guidance
neuron projection guidance
membrane organization
secretion by cell
system process
synaptic vesicle recycling
regulation of secretion by cell
mitochondrial membrane organization
ribonucleotide metabolic process
ribonucleoside triphosphate metabolic process
purine ribonucleoside triphosphate metabolic process
protein localization
mitochondrial outer membrane permeabilization
positive regulation of mitochondrial membrane permeability involved in ap
mitochondrial outer membrane permeabilization involved in programmed
learning
hydrogen ion transmembrane transport
secretion
cellular homeostasis
vesicle-mediated transport
regulation of cation transmembrane transport
ribose phosphate metabolic process
regulation of secretion
purine ribonucleotide metabolic process
mitochondrial transport
synapse assembly
single-organism cellular localization
purine nucleoside triphosphate metabolic process
adult behavior
positive regulation of mitochondrial membrane permeability
protein localization to synapse
purine nucleotide metabolic process
neurogenesis
nucleoside metabolic process
positive regulation of cell projection organization
potassium ion transport
regulation of exocytosis

endomembrane system organization
apoptotic mitochondrial changes
cellular ion homeostasis
calcium ion-dependent exocytosis
modulation of synaptic transmission
proton transport
glycosyl compound metabolic process
regulation of neuron differentiation
gamma-aminobutyric acid signaling pathway
regulation of metal ion transport
cellular cation homeostasis
macromolecule localization
regulation of axonogenesis
hydrogen transport
ferric iron transport
trivalent inorganic cation transport
neurofilament cytoskeleton organization
mitochondrion organization
memory
cation homeostasis
cellular potassium ion transport
potassium ion transmembrane transport
intracellular transport
protein localization to mitochondrion
nucleoside phosphate metabolic process
fibroblast growth factor receptor signaling pathway
single-organism intracellular transport
generation of precursor metabolites and energy
insulin secretion involved in cellular response to glucose stimulus
synaptic vesicle endocytosis
regulation of insulin secretion involved in cellular response to glucose stim
calcium ion transport
response to cocaine
regulation of mitochondrial membrane permeability
divalent metal ion transport
cellular response to fibroblast growth factor stimulus
establishment of protein localization to mitochondrion
protein transport
regulation of cell morphogenesis involved in differentiation
divalent inorganic cation transport
sodium ion transmembrane transport
cellular component organization
insulin receptor signaling pathway

cytoskeleton-dependent intracellular transport
organelle organization
cellular component organization or biogenesis
establishment of protein localization
inorganic ion homeostasis
cellular metal ion homeostasis
microtubule-based transport
developmental cell growth
neuron-neuron synaptic transmission
protein oligomerization
response to fibroblast growth factor
phagosome maturation
regulation of synaptic vesicle transport
nucleotide metabolic process
regulation of membrane permeability
purine-containing compound metabolic process
protein insertion into mitochondrial membrane involved in apoptotic signa
behavioral response to cocaine
positive regulation of mitochondrial outer membrane permeabilization inv
regulation of vesicle-mediated transport
regulation of cation channel activity
neuron projection extension
phosphate-containing compound metabolic process
regulation of neurogenesis
regulation of cellular component organization
acrosome reaction
neurofilament bundle assembly
histone H2A acetylation
intermediate filament bundle assembly
response to acrylamide
transmembrane receptor protein tyrosine kinase signaling pathway
negative regulation of transporter activity
transferrin transport
regulation of transporter activity
phosphorus metabolic process
response to nitrogen compound
single-organism membrane organization
nucleobase-containing small molecule metabolic process
ion homeostasis
glutamate metabolic process
protein insertion into membrane
positive regulation of synaptic transmission
cellular component assembly

cellular response to insulin stimulus
energy derivation by oxidation of organic compounds
vesicle docking
positive regulation of axonogenesis
positive regulation of mitochondrion organization
hormone transport
mitochondrial electron transport, NADH to ubiquinone
negative regulation of cell projection organization
protein insertion into mitochondrial membrane
positive regulation of neurogenesis
metal ion homeostasis
response to organonitrogen compound
response to histamine
NFAT protein import into nucleus
regulation of NFAT protein import into nucleus
cellular response to histamine
regulation of synaptic vesicle recycling
regulation of hormone secretion
calcium-mediated signaling
positive regulation of cell morphogenesis involved in differentiation
response to insulin
epidermal growth factor receptor signaling pathway
chemical homeostasis
organophosphate metabolic process
ERBB signaling pathway
regulation of dendrite development
membrane fusion
hormone secretion
cellular response to nitrogen compound
homophilic cell adhesion via plasma membrane adhesion molecules
adult locomotory behavior
multicellular organismal signaling
cell development
dendrite development
regulation of calcium ion-dependent exocytosis
regulation of potassium ion transmembrane transport
regulation of cell morphogenesis
dopamine secretion
regulation of dopamine secretion
cellular component biogenesis
regulation of establishment of protein localization
neurotrophin TRK receptor signaling pathway
protein complex assembly

protein complex biogenesis
positive regulation of transport
regulation of calcium ion transport
positive regulation of cell development
regulation of intracellular transport
neuromuscular process
insulin secretion
neuronal action potential
positive regulation of organelle organization
membrane docking

Genes
ACTN2 AKAP5 ALDH5A1 AMPH ARHGEF9 CACNB1 CACNB2 CACNB4 CACNG2 CACNG3 CADPS CALB1 CAM
ACTN2 AKAP5 ALDH5A1 AMPH ARHGEF9 CACNB1 CACNB2 CACNB4 CACNG2 CACNG3 CADPS CALB1 CAM
AMIGO1 CALB1 CAMK2A CAMK2B CBLN2 CDC42 CDK5 CHRNB2 CLSTN3 CNTN4 FGF14 FLRT3 FRMPD4 GR
AMPH AP1AR AP3M2 BLOC1S2 CADPS CDK5 DOC2A DYNC1I1 FGF14 KIF3A KIFAP3 MAP2K1 MYO5A NRX
ABCG4 ACSL4 ACTN2 ADD2 AKAP5 ALDH5A1 AMIGO1 AMPH ANO3 ANXA6 AP1AR AP3M2 APOO ARHGEF
ABCG4 ACSL4 ACTN2 ADD2 AKAP5 ALDH5A1 AMIGO1 AMPH ANO3 ANXA6 AP1AR AP3M2 APOO ARHGEF
ABCG4 ACSL4 ACTN2 ADD2 AKAP5 ALDH5A1 AMIGO1 AMPH ANO3 ANXA6 AP1AR AP3M2 APOO ARHGEF
AMPH AP1AR AP3M2 BLOC1S2 CADPS CDK5 DOC2A DYNC1I1 FGF14 KIF3A KIFAP3 MAP2K1 MYO5A PACS
ACADSB ACTN2 ADD2 AKAP5 ALDH5A1 AMIGO1 ANO3 ANXA6 AP1AR APEX1 ARPC5L ARV1 ATP1A1 ATP1
ACTN2 AKAP5 AMIGO1 ANXA6 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1
ACSL4 ACTN2 AKAP5 AMIGO1 ATP1A1 ATP8A2 BAG4 CACNA2D1 CACNB1 CACNB2 CACNB4 CACNG2 CAC
ACSL4 ACTN2 AKAP5 AMIGO1 ATCAY ATL1 ATP8A2 BCL11A BLOC1S2 BMPR2 CACNB1 CACNB2 CACNB4 C
ACTN2 AKAP5 AMIGO1 ATL1 ATP8A2 BCL11A BMPR2 CACNB1 CACNB2 CACNB4 CAMK2A CAMK2B CAMK
ACSL4 ACTN2 AKAP5 AMIGO1 ATCAY ATL1 ATP8A2 BCL11A BLOC1S2 BMPR2 CACNB1 CACNB2 CACNB4 C
ABCG4 ACSL4 ACTN2 ADD2 AKAP5 ALDH5A1 AMIGO1 AMPH ANO3 ANXA6 AP1AR AP3M2 APOO ARHGEF
ACTN2 AKAP5 AMIGO1 ATL1 ATP6V0D1 ATP6V1D ATP8A2 BCL11A BMPR2 CACNB1 CACNB2 CACNB4 CA
AMPH AP3M2 BLOC1S2 CADPS CDK5 DOC2A FGF14 NRXN1 PACSIN1 PCLO PFN2 RAB3A RAB3C RIMS1 RP
ACTN2 AMIGO1 ANO3 ANXA6 ARHGEF9 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP5B ATP5G1 ATP6V0A1 ATP
AFF2 AMPH ATP1A3 CACNB4 CALB1 CAMK4 CDK5 CHRNB2 CNTNAP2 DNM1 ELAVL4 EPHA4 FGF12 FGF13
ACTN2 AMIGO1 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP5B ATP5G1 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1
ACTN2 AKAP5 AMIGO1 ATL1 ATP6V0D1 ATP6V1D ATP8A2 BCL11A BMPR2 CACNB1 CACNB2 CACNB4 CA
ACTN2 AMIGO1 ATL1 ATP8A2 BCL11A BMPR2 CACNB1 CACNB2 CACNB4 CAMK2A CAMK2B CAMK2D CAP
AMPH AP3M2 BLOC1S2 CADPS CDK5 DOC2A FGF14 PACSIN1 PCLO PFN2 RAB3A RAB3C RIMS1 RPH3A SH
AMPH AP3M2 BLOC1S2 CADPS CDK5 DOC2A FGF14 PACSIN1 PCLO PFN2 RAB3A RAB3C RIMS1 RPH3A SH
ACTN2 AKAP5 AMIGO1 ATL1 ATP8A2 BCL11A BMPR2 CACNB1 CACNB2 CACNB4 CAMK2A CAMK2B CAMK
ACTN2 AKAP5 AMIGO1 AP1AR ARPC5L ATP8A2 BAG4 BCL11A BMPR2 CAMK1D CAMK2B CBLN2 CDC42 C
ACSL4 ACTL6B ACTN2 ADAM23 AFF2 AKAP5 ALDH5A1 AMIGO1 ASTN1 ATCAY ATL1 ATP2B1 ATP6AP2 AT
AMPH AP1AR AP3M2 BLOC1S2 CADPS CDC42 CDK5 DOC2A DYNC1I1 FGF14 KIF3A KIFAP3 MAP2K1 MYH1
ACSL4 ACTN2 ADD2 AKAP5 AMIGO1 ANO3 ANXA6 ARHGEF9 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP5B ATP
ABCG4 ACTN2 ADD2 AMIGO1 ANO3 ANXA6 ARHGEF9 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP5B ATP5G1 A
AFF2 AMPH ATP1A3 ATP8A2 CACNB2 CACNB4 CACNG2 CACNG3 CALB1 CAMK2B CAMK4 CDK5 CHRM1 C
AMIGO1 CACNB1 CACNB2 CACNB4 CACNG2 CAMK2B CBLN2 CDC42 CDK5 CHRNB2 CLSTN3 FLRT3 FRMPD
AKAP5 ALDH5A1 CADPS CAMK2A CDK5 CHRM3 DOC2A ENY2 EPHA5 GAD1 GAD2 GLS HTR2A ITPR1 KCNC
ACTN2 AMIGO1 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP5B ATP5G1 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1
ACTN2 AMIGO1 ATL1 ATP8A2 BCL11A BMPR2 CACNB1 CACNB2 CACNB4 CAMK2A CAMK2B CAMK2D CAP
ABCG4 ACSL4 ACTN2 ADD2 AKAP5 ALDH5A1 AMIGO1 AMPH ANO3 ANXA6 AP1AR AP3M2 APOO ARHGEF
ATP1A1 ATP1A3 ATP5B ATP5G1 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1E1 ATP6V1
ATP1A1 ATP1A3 ATP5B ATP5G1 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1E1 ATP6V1
AFF2 AMPH ATP1A3 CALB1 CAMK4 CDK5 CHRM1 CHRNB2 CNTNAP2 ELAVL4 FGF13 GPI GPR155 GRIA1 G
AKAP5 AMIGO1 ATP8A2 BCL11A BMPR2 CAMK1D CAMK2B CDK5 CDKL5 CHN1 CHRNB2 CPNE5 ELAVL4 E

CADPS CDK5 DOC2A PCLO PFN2 RAB3A RAB3C RIMS1 RPH3A SNAP25 STXBP1 SYN1 SYNJ1 SYT1 SYT13 SY
ACTN2 AMIGO1 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP5B ATP5G1 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1
AMPH AP1AR AP3M2 ATCAY BLOC1S2 CADPS CDC42 CDK5 DOC2A DYNC1I1 FGF14 KIF3A KIFAP3 MAP2K1
ACSL4 ACTN2 AKAP5 AMIGO1 ATCAY ATL1 ATP6V0D1 ATP6V1D ATP8A2 BAG4 BCL11A BLOC1S2 BMPR2
AFF2 AMPH ATP1A3 CALB1 CAMK4 CDK5 CHRNB2 CNTNAP2 ELAVL4 FGF13 GPI GRIA1 GRIN2A GRIN2B H
ASTN1 ATP1A3 CACNB4 CALB1 CHRNB2 DNM1 ELAVL4 EPHA4 FGF12 FGF14 FIG4 GLRB HPRT1 KCND2 LR
ACTN2 AKAP5 BAG4 CAMK2A CAMK2D CAMK4 CASQ1 CDC42 CDK5 CHRM1 CHRM3 CHRNB2 DNAJC27 D
ALDH5A1 CADPS CAMK2A CDK5 DOC2A GAD1 GAD2 GLS MEF2C NRXN1 NRXN3 PCLO PFN2 PPT1 RAB3A
AMIGO1 CAMK2B CBLN2 CDC42 CHRNB2 CLSTN3 FLRT3 FRMPD4 LINGO2 LRP4 LRRN3 LRRTM1 LRRTM3 L
ALDH5A1 CADPS CAMK2A CDK5 DOC2A GAD1 GAD2 GLS MEF2C NRXN1 NRXN3 PCLO PFN2 PPT1 RAB3A
ACTN2 AKAP5 AMIGO1 AP1AR ATL1 ATP8A2 BASP1 BCL11A BMPR2 CACNB1 CACNB2 CACNB4 CAMK2A C
AK5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 DLD DLG3 DNM1L ENO2 GPI HK1 HPRT1 HTR2A LDH
AMIGO1 CBLN2 CHRNB2 CLSTN3 FLRT3 LINGO2 LRRN3 LRRTM1 LRRTM3 LRTM2 MEF2C NRXN1 NRXN3 R
ACTN2 AKAP5 AMIGO1 ANXA6 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP5B ATP5G1 ATP6V0A1 ATP6V0D1 AT
ACSL4 ACTN2 AKAP5 AMIGO1 ATP1A1 ATP8A2 CACNA2D1 CACNB1 CACNB2 CACNB4 CACNG2 CACNG3 C
ACTN2 AKAP5 ALDH5A1 AMPH AP1AR AP3M2 ARL1 ARV1 ATP5B ATP5G1 BAG4 BLOC1S2 CACNB1 CADPS
ACTN2 AKAP5 ALDH5A1 AMPH AP1AR AP3M2 ARL1 ARV1 ATCAY ATP5B ATP5G1 ATP6V1D BAG4 BLOC1S
AFF2 AMPH ASTN1 ATP1A3 ATP8A2 BMPR2 CACNB4 CALB1 CAMK1D CAMK4 CDK5 CHRNB2 CNTNAP2 D
AKAP5 AMIGO1 ATP8A2 BCL11A BMPR2 CAMK1D CAMK2B CDKL5 CPNE5 ELAVL4 ENC1 EPHA4 FIG4 GSK3
AKAP5 AMIGO1 ATP8A2 BCL11A BMPR2 CAMK1D CAMK2B CDC42 CDK5 CDKL5 CHN1 CHRNB2 CPNE5 EL
AK5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 DLD DLG3 DNM1L ENO2 GPI HK1 HPRT1 HTR2A LDH
AKAP5 AMIGO1 ATP8A2 BCL11A BMPR2 CAMK1D CAMK2B CBLN2 CDKL5 CLSTN3 CPNE5 ELAVL4 ENC1 E
CALB1 CAMK2A CAMK2B CDK5 CNTN4 FGF14 GRIA1 GRIN2A GRIN2B LRRTM1 MEF2C NCDN NETO1 NPT
ACSL4 ACTN2 AKAP5 AMIGO1 ATCAY ATL1 ATP8A2 BCL11A BLOC1S2 BMPR2 CACNB1 CACNB2 CACNB4 C
ACTN2 AMIGO1 CACNA2D1 CACNB1 CACNB2 CACNB4 CACNG2 CACNG3 CAMK2D DPP10 DPP6 FGF12 FG
AK5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 DLD DLG3 DNM1L ENO2 GPI HK1 HPRT1 HTR2A LDH
AK5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 DLD DLG3 DNM1L ENO2 GPI HK1 HPRT1 HTR2A LDH
ALDH5A1 CADPS CAMK2A CDK5 DOC2A GAD1 GAD2 GLS MEF2C NRXN1 NRXN3 PCLO PDE1B PFN2 PPT1
ACTN2 AMIGO1 CACNA2D1 CACNB1 CACNB2 CACNB4 CACNG2 CACNG3 CAMK2D DPP10 DPP6 FGF12 FG
AMIGO1 CBLN2 CLSTN3 FLRT3 LINGO2 LRRN3 LRRTM1 LRRTM3 LRTM2 NRXN1 NRXN3 SLITRK3 SLITRK4
ACTN2 ATP1A1 CACNB4 CACNG2 CAMK2D CDK5 CHRNB2 DLD DPP6 EHD3 FGF12 FGF14 GABRA1 GABRA
ACTN2 AKAP5 AMIGO1 AP1AR ATL1 ATP6V0D1 ATP6V1D ATP8A2 BASP1 BCL11A BMPR2 CACNB1 CACNB
ABCG4 ABHD10 ACADSB ACLY ACSL4 ACTN2 ACTR10 ADAM11 ADD2 AGK AK5 AKAP5 ALDH5A1 AMIGO1
AK5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 DLD DNM1L ENO2 GPI HK1 HTR2A LDHA NDUFA2 ND
ACSL4 ACTN2 AKAP5 AMIGO1 AP1AR ATCAY ATP1A1 ATP8A2 BAG4 BMPR2 C16orf45 CACNA2D1 CACNB1
ACTN2 AKAP5 AMIGO1 ATP1A1 ATP1A3 ATP5B ATP5G1 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6
ABCG4 ABHD10 ACADSB ACLY ACSL4 ACTL6B ACTN2 ACTR10 ADAM11 ADAM23 ADD2 AFF2 AGK AK5 AK
AKAP5 AMIGO1 ATP8A2 BCL11A BMPR2 C16orf45 CAMK1D CAMK2B CBLN2 CDK5 CDKL5 CHN1 CHRNB2
ACTN2 CADPS CDK5 DOC2A GLRB MYH10 MYO5A NSF PCLO PFN2 PLCB1 PPP3CB RAB27B RAB3A RAB3C
ACTN2 AKAP5 AMIGO1 AP1AR ATL1 ATP6V0D1 ATP6V1D ATP8A2 BASP1 BCL11A BMPR2 CACNB1 CACNB
BLOC1S2 CAMK2A EYA2 GSK3B MOAP1 YWHAB YWHAG YWHAH YWHAZ
ACSL4 ACTN2 AKAP5 AMIGO1 ASTN1 ATCAY ATL1 ATP8A2 BCL11A BLOC1S2 BMPR2 C16orf45 CACNB1 C
ACLY AK5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 DLD DLG3 DNM1L ENO2 GPI HK1 HPRT1 HTR2A

CDK5 CHRNB2 ELAVL4 GABRA1 GABRB2 GABRB3 GABRG2 GRIN2A HOMER1 HTR2A KCNC2 KCNQ3 NEFH
AKAP5 ANXA6 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP5B ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V
ACLY AK5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 DLD DLG3 DNM1L ENO2 GPI HK1 HPRT1 HTR2A
ACLY AK5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 DLD DLG3 DNM1L ENO2 GPI HK1 HPRT1 HTR2A
AKAP5 AMIGO1 ATP8A2 BCL11A BMPR2 CAMK1D CAMK2B CDKL5 CPNE5 ELAVL4 ENC1 EPHA4 FIG4 GSK3
AK5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 DCTPP1 DLD DNM1L ENO2 ENTPD3 GPI HK1 HTR2A L
ACTN2 BMPR2 CACNB1 CACNB2 CACNB4 CAMK2A CAMK2B CAMK2D CAP2 CDC42 CDK5 CHN1 CNTN4 D
ACTN2 BMPR2 CACNB1 CACNB2 CACNB4 CAMK2A CAMK2B CAMK2D CAP2 CDC42 CDK5 CHN1 CNTN4 D
ACTN2 ANO3 APOO ARV1 ATP8A2 BAG4 BLOC1S2 CACNB1 CAMK2A CDK5 CLVS1 CLVS2 CNTNAP2 DLG3
ACTN2 AKAP5 ALDH5A1 CADPS CAMK2A CDK5 CHRM3 CHRNB2 DNM1L DOC2A ENY2 EPHA5 GAD1 GAD2
ACTN2 AFF2 AMPH ANXA6 ATP1A1 ATP1A3 ATP6AP2 ATP8A2 BMPR2 CACNB2 CACNB4 CACNG2 CACNG3
AMPH CDK5 FGF14 PACSIN1 RAB3A SH3GL2 SNCA SYNJ1 SYT1 SYT5
AKAP5 CAMK2A CDK5 CHRM3 CHRNB2 DNM1L DOC2A ENY2 EPHA5 HTR2A ITPR1 KCNA2 KCNC2 MEF2C
APOO BLOC1S2 CAMK2A EYA2 GSK3B IMMT MOAP1 SAMM50 SNCA TOMM22 YWHAB YWHAG YWHAH
ACLY AK5 AKAP5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 CACNB4 CAP2 DLD DLG3 DNM1L ENO2
AK5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 DLD DNM1L ENO2 GPI HK1 HTR2A LDHA NDUFA2 ND
AK5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 DLD DNM1L ENO2 GPI HK1 HTR2A LDHA NDUFA2 ND
ACTN2 AKAP5 AP1AR AP3M2 ARL1 ATCAY ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1
BLOC1S2 EYA2 GSK3B MOAP1 YWHAB YWHAG YWHAH YWHAZ
BLOC1S2 EYA2 GSK3B MOAP1 YWHAB YWHAG YWHAH YWHAZ
BLOC1S2 EYA2 GSK3B MOAP1 YWHAB YWHAG YWHAH YWHAZ
AMPH ATP1A3 CDK5 CHRNB2 CNTNAP2 ELAVL4 FGF13 GRIN2B NDRG4 NETO1 NRXN1 NRXN3 PAK7 PDE1
ATP1A1 ATP1A3 ATP5B ATP5G1 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1E1 ATP6V1
ACSL4 ACTN2 AKAP5 ALDH5A1 CACNB4 CADPS CAMK2A CDK5 CHRM1 CHRM3 CHRNB2 DNM1L DOC2A E
AKAP5 ANXA6 APEX1 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP5B ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2
ACTN2 AMPH AP1AR AP3M2 ARL1 ATP6V1H BLOC1S2 C9orf72 CADPS CAMK1D CDC42 CDK5 CLVS1 CLVS
ACTN2 AMIGO1 CACNB1 CACNB2 CACNB4 CAMK2D DPP10 DPP6 FGF12 FGF14 FXYD7 GNB5 HOMER1 JP
ACLY AK5 AKAP5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 CACNB4 CAP2 DLD DLG3 DNM1L ENO2
ACSL4 AKAP5 CAMK2A CDK5 CHRM3 CHRNB2 DNM1L DOC2A ENY2 EPHA5 HTR2A ITPR1 KCNA2 KCNC2
ACLY AK5 AKAP5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 CACNB4 CAP2 DLD DLG3 DNM1L ENO2
ATP5B ATP5G1 BAG4 BLOC1S2 CAMK2A EPT1 EYA2 FBXW7 GDAP1 GRPEL2 GSK3B MAPK9 MOAP1 MTX3
AMIGO1 CBLN2 CDK5 CHRNB2 CLSTN3 FLRT3 GLRB LINGO2 LRP4 LRRN3 LRRTM1 LRRTM3 LRTM2 MEF2C
ACTN2 AKAP5 AMPH AP3M2 ATCAY BAG4 BLOC1S2 CACNB1 CADPS CDK5 DLG3 DOC2A DPP10 DPP6 DYN
AK5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 DLD DNM1L ENO2 GPI HK1 HTR2A LDHA NDUFA2 ND
ATP1A3 CACNB4 CDK5 CHRNB2 CNTNAP2 DNM1 EPHA4 FGF12 FGF14 GABRG2 GLRB HOMER1 HTR2A NR
BLOC1S2 EYA2 GSK3B MOAP1 YWHAB YWHAG YWHAH YWHAZ
CDK5 CLSTN3 DLG3 HOMER1 LRRTM1 NETO1 NRXN1
ACLY AK5 AKAP5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 CACNB4 CAP2 DLD DLG3 DNM1L ENO2
ACSL4 ACTN2 AKAP5 AMIGO1 ASTN1 ATCAY ATL1 ATP8A2 BCL11A BLOC1S2 BMPR2 C16orf45 CACNB1 C
ACLY AK5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 DLD DLG3 DNM1L ENO2 GPI HK1 HPRT1 HTR2A
AKAP5 AMIGO1 ATP8A2 BCL11A BMPR2 CAMK1D CAMK2B CDC42 CDKL5 CPNE5 ELAVL4 ENC1 EPHA4 FI
ACTN2 AKAP5 AMIGO1 ATP1A1 ATP1A3 DPP10 DPP6 HCN1 HTR2A KCNA2 KCNA4 KCNAB1 KCNAB2 KCNC
CDK5 DOC2A NSF PCLO PFN2 PLCB1 RAB27B RAB3A RAB3C RALB RPH3A SCAMP5 SNCA SNX4 STXBP1 ST

ACTN2 ANO3 ARL1 ARV1 ATL1 BAG4 BLOC1S2 CASQ1 CDC42 DNM1 DPP10 DPP6 EHD2 EHD3 EPB41L3 FG
BLOC1S2 CAMK2A DNM1L EYA2 GGCT GSK3B MAPK9 MLLT11 MOAP1 SLC25A4 YWHAB YWHAG YWHAH
AKAP5 ANXA6 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP5B ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V
CDK5 DOC2A GLRB PLCB1 PPP3CB RIMS1 RPH3A SCAMP5 STXBP1 SYT1 SYT4 SYT5 TRIM36
CALB1 CAMK2A CAMK2B CDK5 CHRNB2 CLSTN3 CNTN4 FGF14 GRIA1 GRIN2A GRIN2B HTR2A LRRTM1 M
ATP1A1 ATP1A3 ATP5B ATP5G1 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1D ATP6V1E
ABHD10 ACLY AK5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 DLD DLG3 DNM1L ENO2 GPI HK1 HPRT
AKAP5 AMIGO1 ATP8A2 BCL11A BMPR2 CAMK1D CAMK2B CDK5 CDKL5 CHN1 CHRNB2 CNTN4 CPNE5 EL
CACNB4 GABBR2 GABRA1 GABRA3 GABRA4 GABRB2 GABRG2 GABRG3
ACTN2 AKAP5 AMIGO1 ATP1A1 CACNA2D1 CACNB1 CACNB2 CACNB4 CAMK2A CAMK2B CAMK2D CASQ1
AKAP5 ANXA6 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP5B ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V
ABCG4 ACSL4 ACTN2 AKAP5 ANO3 AP1AR AP3M2 APOO ARL1 ARV1 ATCAY ATP6V0A1 ATP6V0D1 ATP6V
AMIGO1 BCL11A BMPR2 CDK5 CDKL5 CHN1 EPHA4 FGF13 GSK3B L1CAM LRP4 MAP2K1 NEFL OLFM1 PTP
ATP1A1 ATP1A3 ATP5B ATP5G1 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1D ATP6V1E
ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1D ATP6V1E1 ATP6V1H STEAP2
ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1D ATP6V1E1 ATP6V1H STEAP2
ATP8A2 INA NEFH NEFL NEFM
APOO ATCAY ATP5B BAG4 BLOC1S2 CAMK2A CLVS1 DNM1L EPT1 EYA2 FBXW7 GABARAPL1 GDAP1 GGCT
ATP1A3 CALB1 CAMK4 CHRNB2 FGF13 GRIA1 GRIN2B HTR2A NETO1 PAK7 PJA2 PLCB1 PLK2 PPP3CB RCA
AKAP5 ANXA6 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP5B ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V
ACTN2 AMIGO1 ATP1A1 ATP1A3 DPP10 DPP6 HCN1 KCNA2 KCNA4 KCNAB1 KCNAB2 KCNC2 KCND2 KCN
ACTN2 AMIGO1 ATP1A1 ATP1A3 DPP10 DPP6 HCN1 KCNA2 KCNA4 KCNAB1 KCNAB2 KCNC2 KCND2 KCN
ACTN2 AKAP5 AP1AR AP3M2 ARL1 ARV1 ATP5B ATP5G1 BAG4 BLOC1S2 CACNB1 CAMK2A CAMK2D CAM
BAG4 DNM1L EPT1 FBXW7 GDAP1 GRPEL2 HK1 MAPK9 MOAP1 MTX3 PSMD8 SAMM50 TOMM20 TOMM
ACLY AK5 AKAP5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 CACNB4 CAP2 DCTPP1 DLD DLG3 DNM1
ACTN2 CAMK2A CAMK2B CAMK2D CAMK4 FGF12 GRIN2A GRIN2B GSK3B ITPR1 KRAS MAP2K1 NEFL NPT
ACTN2 AKAP5 AP1AR AP3M2 ARL1 ARV1 ATP5B ATP5G1 BAG4 BLOC1S2 CACNB1 CAMK2A CAMK2D CAM
ACLY AKAP5 ALDH5A1 ATP5B ATP5G1 CHRM3 CISD1 DLD ENO2 FH GNG3 GPI GSK3B HK1 HTR2A ITPR1 KC
ENY2 EPHA5 NRXN1 OXCT1 PPP3CB PRKCE SYBU VSNL1
AMPH CDK5 PACSIN1 SH3GL2 SNCA SYNJ1 SYT1 SYT5
ENY2 EPHA5 NRXN1 OXCT1 PPP3CB PRKCE SYBU VSNL1
AKAP5 ANXA6 ATP2B1 ATP2B3 CACNA2D1 CACNB1 CACNB2 CACNB4 CACNG2 CACNG3 CAMK2A CAMK2
CDK5 CHRNB2 ELAVL4 GRIN2A HOMER1 HTR2A NEFH OPRK1 SNCA
BLOC1S2 CAMK2A EYA2 GSK3B MOAP1 YWHAB YWHAG YWHAH YWHAZ
AKAP5 ANXA6 ATP2B1 ATP2B3 CACNA2D1 CACNB1 CACNB2 CACNB4 CACNG2 CACNG3 CAMK2A CAMK2
ACTN2 CAMK2A CAMK2B CAMK2D CAMK4 FGF12 GRIN2A GRIN2B GSK3B ITPR1 KRAS MAP2K1 NEFL NPT
BAG4 EPT1 FBXW7 GDAP1 GRPEL2 HK1 MAPK9 MOAP1 MTX3 PSMD8 SAMM50 TOMM20 TOMM22 TOM
AKAP5 AP1AR AP3M2 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1D ATP6V1E1 ATP6V1
AKAP5 AMIGO1 AP1AR BCL11A BMPR2 CAMK2B CDC42 CDK5 CDKL5 CHN1 CHRNB2 EPHA4 FGF13 GSK3B
AKAP5 ANXA6 ATP2B1 ATP2B3 CACNA2D1 CACNB1 CACNB2 CACNB4 CACNG2 CACNG3 CAMK2A CAMK2
ATP1A1 ATP1A3 CAMK2D FGF12 FXYD7 HCN1 PRKCE SCN1A SCN2A SCN4B SCN8A SLC4A10 SLC4A8 SLC8
ACSL4 ACTL6B ACTN2 ADD2 AKAP5 ALDH5A1 AMIGO1 ANO3 ANXA6 AP1AR APEX1 APOO ARL1 ARPC5L A
ACTN2 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1D ATP6V1E1 ATP6V1H CAMK2A CA

AP3M2 BLOC1S2 CDC42 DYNC1I1 KIF3A KIFAP3 MAP2K1 NEFH NEFL RASGRP1 SSX2IP TUBB UCHL1
ACTL6B ACTN2 ADD2 AP1AR APEX1 APOO ARL1 ARPC5L ASH2L ATCAY ATL1 ATP5B ATP6V0A1 ATP6V0D1
ACSL4 ACTL6B ACTN2 ADD2 AKAP5 ALDH5A1 AMIGO1 ANO3 ANXA6 AP1AR APEX1 APOO ARL1 ARPC5L A
ACTN2 AKAP5 AP1AR AP3M2 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1D ATP6V1E1
AKAP5 ANXA6 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP5B ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V
AKAP5 ANXA6 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 AT
AP3M2 BLOC1S2 CDC42 DYNC1I1 KIF3A KIFAP3 MAP2K1 NEFH NEFL RASGRP1 SSX2IP UCHL1
BCL11A BMPR2 CAMK2D CDK5 CDKL5 CPNE5 DCLK1 DCX FGF13 FLRT3 GSK3B L1CAM OLFM1 PIN1 PPP3C
CACNB4 CAMK4 CDH8 CDK5 CHRNB2 CLSTN3 DNM1 GABRA1 GABRB2 GABRG2 GLRB GRIA1 GRIA3 GRIN2
ACTN2 ALDH5A1 ANXA6 ATL1 BCL11A CAMK2D CHRNB2 DCTPP1 DNM1 DNM1L EHD3 FH GLRB GLS GRIN
ACTN2 CAMK2A CAMK2B CAMK2D CAMK4 FGF12 GRIN2A GRIN2B GSK3B ITPR1 KRAS MAP2K1 NEFL NPT
ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1D ATP6V1E1 ATP6V1H
CDK5 FGF14 PFN2 RAB3A SNCA STXBP1 SYN1 SYNJ1
ACLY AK5 AKAP5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 CACNB4 CAP2 DLD DLG3 DNM1L DPM1
BLOC1S2 CAMK2A EYA2 GSK3B MOAP1 YWHAB YWHAG YWHAH YWHAZ
ACLY AK5 AKAP5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 CACNB4 CAP2 DLD DLG3 DNM1L ENO2
MOAP1 YWHAB YWHAG YWHAH YWHAZ
CDK5 HOMER1 HTR2A OPRK1 SNCA
GSK3B YWHAB YWHAG YWHAH YWHAZ
ACTN2 CAMK1D CDK5 DOC2A EHD2 FGF14 LRRTM1 MAP2K1 NDRG4 NSF PACSIN1 PCLO PFN2 PLCB1 PPT
ACTN2 CACNB1 CACNB2 CACNB4 CAMK2D FGF12 FGF14 GNB5 HOMER1 JPH1 KCNAB1 MYO5A
BCL11A BMPR2 CDK5 CDKL5 CPNE5 DCLK1 DCX FLRT3 GSK3B L1CAM OLFM1 PPP3CB RIMS1 SLC9A6 SLIT2
ACLY ACTN2 AGK AK5 AKAP5 ALDH5A1 ATP1A1 ATP5B ATP5G1 ATP6AP2 ATP6V0A1 ATP6V1A ATP6V1B2
AKAP5 AMIGO1 ATP8A2 BCL11A BMPR2 C16orf45 CAMK1D CAMK2B CDK5 CDKL5 CHN1 CHRNB2 CNTN4
ACSL4 ACTN2 ADD2 AKAP5 AMIGO1 AP1AR ARPC5L ATP8A2 BAG4 BCL11A BMPR2 C16orf45 CAMK1D CA
GLRB PLCB1 TRIM36
NEFH NEFL NEFM
MEAF6 MORF4L2 YEATS4
NEFH NEFL NEFM
NEFH NEFL OPRK1
ACTN2 ARHGEF9 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1D ATP6V1E1 ATP6V1H BM
ACTN2 CAMK2D FGF12 GNB5 KCNAB1 NDFIP2 PRKCE SNCA
ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1D ATP6V1E1 ATP6V1H
ACTN2 CACNB1 CACNB2 CACNB4 CACNG2 CACNG3 CAMK2D FGF12 FGF14 FXYD7 GNB5 HOMER1 JPH1 K
ACLY ACSL4 ACTN2 AGK AK5 AKAP5 ALDH5A1 ATP1A1 ATP5B ATP5G1 ATP6AP2 ATP6V0A1 ATP6V1A ATP
ACTN2 AKAP5 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1D ATP6V1E1 ATP6V1H CAMK
ACTN2 ANO3 APOO ARV1 ATP8A2 BAG4 BLOC1S2 CACNB1 CAMK2A CDK5 CNTNAP2 DLG3 DNM1L DPP1
ACLY AK5 AKAP5 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 CACNB4 CAP2 DCTPP1 DLD DLG3 DNM1
AKAP5 ANXA6 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP5B ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V
ALDH5A1 ATCAY GAD1 GAD2 GLS GOT1
MOAP1 REEP1 YWHAB YWHAG YWHAH YWHAZ
CHRNB2 CLSTN3 GRIN2B LRRTM1 NETO1 NPTN NRXN1 PLK2 PRKCE RASGRF2 RIMS1 SNAP25 SNCA SYNJ1
ACTN2 ADD2 ALDH5A1 AMIGO1 ANXA6 ARPC5L ATL1 ATP6V0A1 ATP6V0D1 ATP6V1D BAG4 BCL11A BLO

ACTN2 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1D ATP6V1E1 ATP6V1H CAMK2A CAM
ACLY AKAP5 ALDH5A1 ATP5B ATP5G1 CHRM3 CISD1 DLD FH GNG3 GSK3B ITPR1 KCNC2 MDH1 MRAP2 N
NDRG4 NSF RAB27B RAB3A RAB3C RALB SNAP25 STXBP1 UNC13A VPS33B
AMIGO1 BCL11A BMPR2 CDKL5 GSK3B L1CAM MAP2K1 NEFL ROBO2 SLIT2
DNM1L EPT1 FBXW7 GSK3B HK1 MLLT11 MOAP1 PSMD8 STOML2 UGCG YWHAB YWHAG YWHAH YWHA
AKAP5 CHRM3 CRYM ENY2 EPHA5 HTR2A ITPR1 KCNC2 MYO5A NRXN1 OPRK1 OXCT1 PCLO PPP3CA PPP3
DLD NDUFA2 NDUFA5 NDUFA6 NDUFAB1 NDUFB5 SNCA
BCL11A CDK5 EPHA4 FGF13 GSK3B LRP4 NRXN1 PFN2 PLK2 PPP3CA PTPRO SLIT2 STMN2 TBC1D30 THY1 Y
MOAP1 YWHAB YWHAG YWHAH YWHAZ
AKAP5 AMIGO1 ATP8A2 BCL11A BMPR2 CAMK1D CAMK2B CDKL5 CPNE5 ELAVL4 ENC1 EPHA4 FIG4 FZD3
AKAP5 ANXA6 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 AT
ACTN2 AKAP5 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1D ATP6V1E1 ATP6V1H CAMK
GABRA1 GABRB2 GABRB3 GABRG2
AKAP5 GSK3B PPP3CA PPP3CB
AKAP5 GSK3B PPP3CA PPP3CB
GABRA1 GABRB2 GABRB3 GABRG2
CDK5 FGF14 SNCA SYNJ1
AKAP5 CHRM3 ENY2 EPHA5 HTR2A ITPR1 KCNC2 NRXN1 OPRK1 OXCT1 PPP3CA PPP3CB PRKAR2B PRKCE
CAMK2D CAMKK2 CASQ1 HPCA ITPR1 L1CAM MCTP1 NCALD PPP3CA PPP3CB RCAN2 SLC8A1
AKAP5 AMIGO1 BCL11A BMPR2 CAMK2B CDC42 CDKL5 EPHA4 GSK3B L1CAM MAP2K1 MAPK9 NEFL OLF
ACTN2 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1D ATP6V1E1 ATP6V1H CAMK2A CAM
ACTN2 CAMK2A CAMK2B CAMK2D CAMK4 CDC42 FBXW7 GRIN2A GRIN2B GSK3B ITPR1 KRAS MAP2K1 N
ACADSB AKAP5 ANXA6 ATP1A1 ATP1A3 ATP2B1 ATP2B3 ATP5B ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B
ACLY AK5 AKAP5 ALDH5A1 ATP5B ATP5G1 ATP6V0A1 ATP6V1A ATP6V1B2 CACNB4 CAP2 CDC42 DCTPP1
ACTN2 CAMK2A CAMK2B CAMK2D CAMK4 CDC42 FBXW7 GRIN2A GRIN2B GSK3B ITPR1 KRAS LGMN MA
AKAP5 BCL11A CAMK1D CAMK2B CDK5 CDKL5 CHRNB2 ELAVL4 EPHA4 MEF2C PACSIN1 PAK3 PLK2 PPP3
DNM1L GABARAPL1 GDAP1 NAPB NAPG NSF RAB3A RIMS1 SNAP25 STOML2 STXBP1 SYT4 UBXN2B VAM
AKAP5 CHRM3 ENY2 EPHA5 HTR2A ITPR1 KCNC2 MYO5A NRXN1 OPRK1 OXCT1 PCLO PPP3CA PPP3CB PR
ACTN2 AKAP5 ATP6V0A1 ATP6V0D1 ATP6V1A ATP6V1B2 ATP6V1C1 ATP6V1D ATP6V1E1 ATP6V1H CAMK
AMIGO1 CADM3 CD200 CDH10 CDH12 CDH18 CDH8 CLSTN3 FAT3 L1CAM NPTN PCDH7 ROBO2
ATP1A3 CACNB4 DNM1 EPHA4 FGF12 FGF14 GLRB OXR1 PPT1 SCN1A SCN8A SNCA UCHL1
ATP1A1 ATP1A3 CACNB4 CACNG2 CACNG3 CAMK2D CNTNAP2 DPP6 KCNA2 KCND2 SCN1A SCN2A SCN4
ACSL4 ACTN2 AKAP5 AMIGO1 AP1AR ATCAY ATL1 ATP8A2 BASP1 BCL11A BLOC1S2 BMPR2 C16orf45 CAC
ACSL4 AKAP5 BCL11A CAMK1D CAMK2B CDK5 CDKL5 CHRNB2 DCLK1 DCX ELAVL4 EPHA4 HPRT1 LRP4 MA
CDK5 DOC2A PLCB1 RPH3A SCAMP5 STXBP1 SYT1 SYT4 SYT5
ACTN2 AMIGO1 DPP10 DPP6 KCNAB1 KCNAB2 KCNC2 KCNIP4 OPRK1
AKAP5 AMIGO1 AP1AR BCL11A BMPR2 CAMK2B CDC42 CDK5 CDKL5 CHN1 CHRNB2 CPNE5 EPB41L3 EPH
CHRNB2 HTR2A KCNA2 OPRK1 SNCA
CHRNB2 HTR2A KCNA2 OPRK1 SNCA
ACTN2 ADD2 ALDH5A1 AMIGO1 ANXA6 ARPC5L ATL1 ATP6V0A1 ATP6V0D1 ATP6V1D BAG4 BCL11A BLO
AKAP5 BAG4 CAMK4 CDC42 CDK5 CHRM1 CHRM3 DNAJC27 DNM1L DPP10 ENY2 EPHA5 EPT1 ERLEC1 FB
ACTN2 ARHGEF9 CAMK2A CAMK2B CAMK2D CAMK4 GRIN2A GRIN2B GSK3B ITPR1 KRAS MAP2K1 MEF2
ACTN2 ADD2 ALDH5A1 ANXA6 ARPC5L ATL1 ATP6V0A1 BAG4 BCL11A BLOC1S2 CADPS CAMK2D CASQ1 C

ACTN2 ADD2 ALDH5A1 ANXA6 ARPC5L ATL1 ATP6V0A1 BAG4 BCL11A BLOC1S2 CADPS CAMK2D CASQ1 C
ACTN2 AKAP5 AMIGO1 ATP8A2 CACNB2 CAMK1D CAMK2A CAMK4 CDC42 CDK5 CHRM1 CHRNB2 DNM1L
AKAP5 CACNA2D1 CACNB1 CACNB2 CACNB4 CAMK2A CAMK2B CAMK2D CASQ1 FGF14 GNB5 HOMER1 J
AKAP5 AMIGO1 ATP8A2 BCL11A BMPR2 CAMK1D CAMK2B CDC42 CDKL5 CPNE5 ELAVL4 ENC1 EPHA4 FIG
ACTN2 AKAP5 BAG4 CAMK2D CAMK4 CASQ1 CDC42 CDK5 CHRM1 DNAJC27 EHD2 EPT1 ERLEC1 FBXW7 G
ATP8A2 CAMK2B FGF12 FGF14 GLRB GRIN2B KCNAB2 MYH10 NEFL NRXN1 SCN1A SCN8A UCHL1
AKAP5 CHRM3 ENY2 EPHA5 ITPR1 KCNC2 MYO5A NRXN1 OXCT1 PCLO PPP3CA PPP3CB PRKAR2B PRKCE
DPP6 KCNA2 KCND2 SCN1A SCN2A SCN8A
ACTN2 AP1AR ARPC5L BAG4 CAMK2B CDK5 DHX36 DNM1L DSTN EPT1 FBXW7 GSK3B HK1 MLLT11 MOA
NDRG4 NSF RAB27B RAB3A RAB3C RALB SNAP25 STXBP1 UNC13A VPS33B

padjust
8.26E-10
3.84E-07
1.15E-06
4.01E-06
4.01E-06
4.74E-06
6.78E-06
1.13E-05
1.21E-05
1.29E-05
1.73E-05
2.02E-05
2.25E-05
2.27E-05
2.77E-05
2.82E-05
2.82E-05
2.90E-05
2.98E-05
4.85E-05
5.16E-05
5.16E-05
5.90E-05
5.90E-05
6.93E-05
6.93E-05
0.00011248
0.00011416
0.00012851
0.00013328
0.0001977
0.00020833
0.00022041
0.00026521
0.00026521
0.00035924
0.00041829
0.00041829
0.00047493
0.00047493

0.00047493
0.00047493
0.00052736
0.00054248
0.00060829
0.00062451
0.00064403
0.00064403
0.00064403
0.00064481
0.00073598
0.0008929
0.00090212
0.00090212
0.00102022
0.0010358
0.00103622
0.00113172
0.00113666
0.00124233
0.00179252
0.0018168
0.00195898
0.00199744
0.00203725
0.00210156
0.0022848
0.00277844
0.00359023
0.00391515
0.00405996
0.00465478
0.00497379
0.00497379
0.00502995
0.00531027
0.00576102
0.00592243
0.00627912
0.00672617
0.00771697
0.00771697
0.00853081

0.00859594
0.00859594
0.0095371
0.0095371
0.0095371
0.0095371
0.0095371
0.0095371
0.00968899
0.00968899
0.00998011
0.01002325
0.01029237
0.01060505
0.01062425
0.01158024
0.01158024
0.01207212
0.0127106
0.0127106
0.0127106
0.01329287
0.0134676
0.01405021
0.01432128
0.01503322
0.01601394
0.01635916
0.01645332
0.01669016
0.01743197
0.01743197
0.01743197
0.0184269
0.02012792
0.02078211
0.02328937
0.02537848
0.02590152
0.02619014
0.02619014
0.02651409
0.0284749

0.02961077
0.02970534
0.03061633
0.03101779
0.03158819
0.03158819
0.03199624
0.03199624
0.03199624
0.03425243
0.03425243
0.03502391
0.03502391
0.03672147
0.03672147
0.03672147
0.03672147
0.03672147
0.03672147
0.03672147
0.03672147
0.03672147
0.03680023
0.03984898
0.04128305
0.04181145
0.04539738
0.04539738
0.04539738
0.04539738
0.04539738
0.04788813
0.05072952
0.05072952
0.05128906
0.05161618
0.0523812
0.05625966
0.05625966
0.05625966
0.05631499
0.05658493
0.05709313

0.05714292
0.05761296
0.05761296
0.05764126
0.06011719
0.06023731
0.06051276
0.06133147
0.06137579
0.06159586
0.06159586
0.06159586
0.06159586
0.06427281
0.06514368
0.06685789
0.06685789
0.06685789
0.06685789
0.07422674
0.07422674
0.07753691
0.0781258
0.07855393
0.07855393
0.07855393
0.07855393
0.07855393
0.07855393
0.07855393
0.08118018
0.08378851
0.08378851
0.08480576
0.08776358
0.08777203
0.08802982
0.08802982
0.09136836
0.09555602
0.09555602
0.09669031
0.09669031

0.09815748
0.10295167
0.1040552
0.1040552
0.10423905
0.10805433
0.10825075
0.11226549
0.11226549
0.11226549
0.11415992
0.11474072
0.11634453
0.11634453
0.11634453
0.11634453
0.11634453
0.11939297
0.13067423
0.1308614
0.13981152
0.13981152
0.14459531
0.14459531
0.14734603
0.14836928
0.14836928
0.1507216
0.16400934
0.16607415
0.16607415
0.17484961
0.17484961
0.17484961
0.17484961
0.17484961
0.17484961
0.17484961
0.17484961
0.17648967
0.17896629
0.17896629
0.17981299

0.17981299
0.1859282
0.18597879
0.18782155
0.18782155
0.18878944
0.18878944
0.18967487
0.18967487
0.18967487

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0006955	7.83E-22	12.6355337	6.5448505	38	394
GO:0002376	2.63E-18	9.01786352	11.0465116	43	665
GO:0002684	1.44E-17	12.1829457	4.03654485	28	243
GO:0006952	1.55E-16	8.81990521	7.59136213	35	457
GO:0006954	8.99E-16	14.0403944	2.54152824	22	153
GO:0002682	3.09E-15	8.43896976	6.77740864	32	408
GO:0045321	6.88E-15	12.5507991	2.79069767	22	168
GO:0002274	1.84E-14	28.5277778	0.83056478	14	50
GO:0002252	1.87E-14	11.1653216	3.27242525	23	197
GO:0002443	3.86E-13	21.7925532	1.01328904	14	61
GO:0001775	6.90E-13	8.75760403	4.26910299	24	257
GO:0050776	8.93E-13	8.63964628	4.31893688	24	260
GO:0050778	2.62E-12	10.1579618	2.94019934	20	177
GO:0002694	1.68E-11	13.8545455	1.57807309	15	95
GO:0002507	1.69E-11	Inf	0.09966777	6	6
GO:0002703	1.91E-11	34.3666667	0.49833887	10	30
GO:0045087	3.57E-11	7.40135773	4.65116279	23	280
GO:0050865	5.63E-11	12.5702479	1.71096346	15	103
GO:0002699	1.09E-10	27.46	0.58139535	10	35
GO:0006950	1.47E-10	4.82735264	17.7906977	43	1071
GO:0046649	2.88E-10	10.0217865	2.24252492	16	135
GO:0002695	3.06E-10	32.0319241	0.46511628	9	28
GO:0002886	4.08E-10	76.6296296	0.21594684	7	13
GO:0002449	4.72E-10	22.8555556	0.66445183	10	40
GO:0002263	5.20E-10	18.2090395	0.88039867	11	53
GO:0002366	5.20E-10	18.2090395	0.88039867	11	53
GO:0002460	7.98E-10	21.4166667	0.69767442	10	42
GO:0032945	8.05E-10	65.6666667	0.23255814	7	14
GO:0050672	8.05E-10	65.6666667	0.23255814	7	14
GO:0006959	1.18E-09	26.4354954	0.53156146	9	32
GO:0002250	1.45E-09	16.2520736	0.96345515	11	58
GO:0050866	1.60E-09	25.3278689	0.54817276	9	33
GO:0002253	1.73E-09	8.73202614	2.52491694	16	152
GO:0002275	2.29E-09	33.2903226	0.3986711	8	24
GO:0070664	2.61E-09	51.0493827	0.26578073	7	16
GO:0042110	5.34E-09	10.6354104	1.66112957	13	100
GO:0070489	5.34E-09	10.6354104	1.66112957	13	100
GO:0071593	5.34E-09	10.6354104	1.66112957	13	100
GO:0050900	7.73E-09	10.2732943	1.71096346	13	103
GO:0050670	8.11E-09	20.2327869	0.64784053	9	39

GO:0046651	9.15E-09	15.8953488	0.88039867	10	53
GO:0070486	9.83E-09	10.0450038	1.74418605	13	105
GO:0032944	1.03E-08	19.575357	0.66445183	9	40
GO:0032943	1.11E-08	15.530303	0.89700997	10	54
GO:0031347	1.26E-08	6.98258345	3.30564784	17	199
GO:0033006	1.44E-08	64.65625	0.19933555	6	12
GO:0043304	1.44E-08	64.65625	0.19933555	6	12
GO:0002683	1.45E-08	10.9278997	1.47840532	12	89
GO:0070663	2.05E-08	17.8351013	0.71428571	9	43
GO:0070661	2.29E-08	14.2222222	0.96345515	10	58
GO:0048584	2.38E-08	4.45887446	9.41860465	28	567
GO:0043300	2.65E-08	55.40625	0.21594684	6	13
GO:0007159	2.72E-08	9.12958138	1.89368771	13	114
GO:0001817	3.36E-08	8.94787941	1.9269103	13	116
GO:0002697	4.42E-08	9.76263031	1.62790698	12	98
GO:0002521	5.08E-08	8.60485325	1.99335548	13	120
GO:0016064	5.11E-08	28.6666667	0.3820598	7	23
GO:0019724	7.12E-08	26.9738562	0.3986711	7	24
GO:0033003	7.52E-08	43.0729167	0.24916944	6	15
GO:0002696	8.35E-08	12.1666667	1.09634551	10	66
GO:0009617	9.70E-08	9.01223582	1.74418605	12	105
GO:0002444	9.76E-08	25.4691358	0.41528239	7	25
GO:0051250	9.76E-08	25.4691358	0.41528239	7	25
GO:0032101	1.04E-07	5.9490922	3.80398671	17	229
GO:0050867	1.12E-07	11.7413793	1.12956811	10	68
GO:0009611	1.16E-07	5.10697674	5.33222591	20	321
GO:0030595	1.19E-07	14.0712924	0.86378738	9	52
GO:1903305	1.19E-07	38.75625	0.26578073	6	16
GO:0002520	1.32E-07	6.20027435	3.40531561	16	205
GO:0034109	1.33E-07	7.84990253	2.15946844	13	130
GO:0050896	1.66E-07	4.32502667	37.2923588	58	2245
GO:0001816	2.28E-07	7.45585508	2.25913621	13	136
GO:0002279	2.68E-07	32.28125	0.29900332	6	18
GO:0002706	2.68E-07	32.28125	0.29900332	6	18
GO:0043303	2.68E-07	32.28125	0.29900332	6	18
GO:0002448	3.87E-07	29.7908654	0.31561462	6	19
GO:0048583	5.26E-07	3.43683703	16.8106312	36	1012
GO:0001819	5.42E-07	9.7	1.32890365	10	80
GO:0051249	6.10E-07	9.56103286	1.34551495	10	81
GO:0032418	1.02E-06	24.1875	0.3654485	6	22
GO:0045576	1.02E-06	24.1875	0.3654485	6	22
GO:0042098	1.20E-06	16.3333333	0.58139535	7	35
GO:0097028	1.27E-06	39.7692308	0.21594684	5	13

GO:0043299	1.37E-06	22.7591912	0.3820598	6	23
GO:0050777	1.37E-06	22.7591912	0.3820598	6	23
GO:0006897	1.85E-06	5.63636364	3.15614618	14	190
GO:0002757	2.48E-06	6.43945469	2.34219269	12	141
GO:0048534	2.86E-06	5.41120219	3.27242525	14	197
GO:0002705	2.89E-06	31.8	0.24916944	5	15
GO:0032844	3.03E-06	6.96735719	1.97674419	11	119
GO:0060326	3.74E-06	8.84378014	1.27906977	9	77
GO:0048872	3.82E-06	10.5651613	0.96345515	8	58
GO:0071219	4.38E-06	13.0444444	0.69767442	7	42
GO:0002513	4.39E-06	Inf	0.04983389	3	3
GO:0002714	4.39E-06	Inf	0.04983389	3	3
GO:0002891	4.39E-06	Inf	0.04983389	3	3
GO:0043207	4.60E-06	5.17408377	3.40531561	14	205
GO:0051707	4.60E-06	5.17408377	3.40531561	14	205
GO:0001773	4.65E-06	62.7272727	0.13289037	4	8
GO:0002712	4.65E-06	62.7272727	0.13289037	4	8
GO:0002889	4.65E-06	62.7272727	0.13289037	4	8
GO:0042129	4.78E-06	17.5653409	0.46511628	6	28
GO:0050727	4.96E-06	10.1538462	0.99667774	8	60
GO:0002573	5.64E-06	9.95982958	1.01328904	8	61
GO:0001906	5.80E-06	26.4871795	0.28239203	5	17
GO:0009607	6.10E-06	5.03571429	3.48837209	14	210
GO:0016477	6.50E-06	3.95194156	6.24584718	19	376
GO:1902105	7.22E-06	9.59296188	1.04651163	8	63
GO:0033993	7.34E-06	4.66256451	4.05315615	15	244
GO:0050863	8.14E-06	9.41935484	1.06312292	8	64
GO:0071216	8.23E-06	11.6951567	0.7641196	7	46
GO:0097529	8.23E-06	11.6951567	0.7641196	7	46
GO:0002455	8.27E-06	50.169697	0.14950166	4	9
GO:0002708	8.27E-06	50.169697	0.14950166	4	9
GO:0051272	8.82E-06	6.88095238	1.79401993	10	108
GO:0045055	8.98E-06	15.44625	0.51495017	6	31
GO:1903706	9.47E-06	7.7928465	1.42857143	9	86
GO:0030098	1.03E-05	9.09010011	1.09634551	8	66
GO:0030097	1.04E-05	5.1116067	3.15614618	13	190
GO:0002822	1.06E-05	22.6923077	0.31561462	5	19
GO:0032845	1.10E-05	11.1192412	0.79734219	7	48
GO:0006909	1.15E-05	8.93384363	1.11295681	8	67
GO:1903037	1.15E-05	8.93384363	1.11295681	8	67
GO:0031349	1.32E-05	6.53883495	1.87707641	10	113
GO:0002821	1.36E-05	41.7979798	0.16611296	4	10
GO:0002824	1.36E-05	41.7979798	0.16611296	4	10

GO:0048870	1.49E-05	3.70091572	6.61129568	19	398
GO:0051674	1.49E-05	3.70091572	6.61129568	19	398
GO:0016337	1.54E-05	4.90846682	3.27242525	13	197
GO:0034110	1.60E-05	8.49531738	1.1627907	8	70
GO:0002700	1.81E-05	19.8461538	0.34883721	5	21
GO:0002819	1.81E-05	19.8461538	0.34883721	5	21
GO:0009605	1.86E-05	3.05771131	12.1760797	27	733
GO:0002262	1.88E-05	13.3028017	0.58139535	6	35
GO:0008285	1.92E-05	4.7991788	3.33887043	13	201
GO:1903034	1.97E-05	7.04551591	1.56146179	9	94
GO:0006956	2.11E-05	35.8181818	0.18272425	4	11
GO:0042130	2.11E-05	35.8181818	0.18272425	4	11
GO:0032103	2.20E-05	8.09727047	1.21262458	8	73
GO:0042060	2.35E-05	4.41666667	3.92026578	14	236
GO:0040011	2.53E-05	3.20447235	9.50166113	23	572
GO:0002685	2.62E-05	12.4385081	0.61461794	6	37
GO:0051704	2.87E-05	3.24407083	8.88704319	22	535
GO:0080134	2.97E-05	3.61644709	6.31229236	18	380
GO:0060627	3.03E-05	5.33220339	2.50830565	11	151
GO:0030099	3.53E-05	6.4982181	1.67774086	9	101
GO:0032496	3.94E-05	7.40208996	1.31229236	8	79
GO:0030335	4.13E-05	6.35681897	1.71096346	9	103
GO:2000147	4.13E-05	6.35681897	1.71096346	9	103
GO:0098602	4.14E-05	4.4277072	3.58803987	13	216
GO:0071222	4.16E-05	11.3327206	0.66445183	6	40
GO:0002237	4.32E-05	7.29749104	1.32890365	8	80
GO:0051251	4.42E-05	8.74358974	0.98006645	7	59
GO:0002702	4.46E-05	27.8451178	0.21594684	4	13
GO:0016192	4.64E-05	3.37464306	7.15946844	19	431
GO:0002286	6.17E-05	25.0545455	0.23255814	4	14
GO:0002532	6.17E-05	25.0545455	0.23255814	4	14
GO:0002718	6.17E-05	25.0545455	0.23255814	4	14
GO:0042116	6.17E-05	25.0545455	0.23255814	4	14
GO:0072376	6.17E-05	25.0545455	0.23255814	4	14
GO:0045088	6.48E-05	5.96655738	1.81063123	9	109
GO:0051239	6.58E-05	2.84349101	12.2757475	26	739
GO:0040017	7.48E-05	5.8466731	1.84385382	9	111
GO:0030334	7.58E-05	4.42758621	3.27242525	12	197
GO:0048518	7.91E-05	2.57175698	25.0996678	41	1511
GO:0002764	7.96E-05	4.40266963	3.28903654	12	198
GO:0002688	8.00E-05	13.7826087	0.46511628	5	28
GO:0001909	8.30E-05	22.7713499	0.24916944	4	15
GO:0042742	9.54E-05	13.2051282	0.48172757	5	29

GO:0022407	0.00010942	6.31325301	1.51162791	8	91
GO:0034097	0.00012238	4.18992042	3.43853821	12	207
GO:2000145	0.00014048	4.12330199	3.48837209	12	210
GO:0050868	0.0001412	19.2587413	0.28239203	4	17
GO:0002888	0.00014653	46.3432836	0.11627907	3	7
GO:0010575	0.00014653	46.3432836	0.11627907	3	7
GO:0043011	0.00014653	46.3432836	0.11627907	3	7
GO:0050878	0.00014701	4.10154219	3.50498339	12	211
GO:0002285	0.00015564	11.7293447	0.53156146	5	32
GO:0002440	0.00015564	11.7293447	0.53156146	5	32
GO:0098609	0.00015859	3.82825088	4.08637874	13	246
GO:0051270	0.00016522	3.81091618	4.10299003	13	247
GO:0051716	0.00017534	2.49709756	31.7607973	47	1912
GO:0002367	0.00017928	17.8787879	0.29900332	4	18
GO:0032675	0.00017928	17.8787879	0.29900332	4	18
GO:1903038	0.00017928	17.8787879	0.29900332	4	18
GO:0045807	0.00018108	11.3076923	0.54817276	5	33
GO:0046849	0.00018108	11.3076923	0.54817276	5	33
GO:0007596	0.00018493	4.27951406	3.05647841	11	184
GO:0007599	0.00020354	4.22847458	3.089701	11	186
GO:0050817	0.00020354	4.22847458	3.089701	11	186
GO:0032635	0.00022425	16.6828283	0.31561462	4	19
GO:0006898	0.00022652	6.56199678	1.26245847	7	76
GO:0006958	0.00023165	37.0656716	0.13289037	3	8
GO:0010574	0.00023165	37.0656716	0.13289037	3	8
GO:0002429	0.0002612	5.49949066	1.71096346	8	103
GO:0001794	0.00027206	Inf	0.03322259	2	2
GO:0001796	0.00027206	Inf	0.03322259	2	2
GO:0001798	0.00027206	Inf	0.03322259	2	2
GO:0002445	0.00027206	Inf	0.03322259	2	2
GO:0002524	0.00027206	Inf	0.03322259	2	2
GO:0002883	0.00027206	Inf	0.03322259	2	2
GO:0002885	0.00027206	Inf	0.03322259	2	2
GO:0002887	0.00027206	Inf	0.03322259	2	2
GO:0002892	0.00027206	Inf	0.03322259	2	2
GO:0002894	0.00027206	Inf	0.03322259	2	2
GO:0007182	0.00027206	Inf	0.03322259	2	2
GO:0014900	0.00027206	Inf	0.03322259	2	2
GO:0033007	0.00027206	Inf	0.03322259	2	2
GO:0034756	0.00027206	Inf	0.03322259	2	2
GO:0043301	0.00027206	Inf	0.03322259	2	2
GO:0043305	0.00027206	Inf	0.03322259	2	2
GO:0045066	0.00027206	Inf	0.03322259	2	2

GO:1903306	0.00027206	Inf	0.03322259	2	2
GO:0006928	0.00027311	2.71780936	10.2990033	22	620
GO:0002761	0.00027673	10.2059553	0.59800664	5	36
GO:0050864	0.00027682	15.6363636	0.33222591	4	20
GO:0070887	0.00027945	2.55655527	13.3554817	26	804
GO:0045637	0.00028541	7.67625	0.93023256	6	56
GO:0050920	0.00028541	7.67625	0.93023256	6	56
GO:0042127	0.00031764	3.01896274	6.89368771	17	415
GO:0051240	0.00033647	3.00226415	6.9269103	17	417
GO:0002690	0.00033768	14.7130125	0.34883721	4	21
GO:0030593	0.00033768	14.7130125	0.34883721	4	21
GO:0034103	0.00033768	14.7130125	0.34883721	4	21
GO:0034111	0.00033768	14.7130125	0.34883721	4	21
GO:1990266	0.00033768	14.7130125	0.34883721	4	21
GO:0002704	0.00034334	30.880597	0.14950166	3	9
GO:0010573	0.00034334	30.880597	0.14950166	3	9
GO:0030851	0.00034334	30.880597	0.14950166	3	9
GO:0036314	0.00034334	30.880597	0.14950166	3	9
GO:0045646	0.00034334	30.880597	0.14950166	3	9
GO:0070723	0.00034334	30.880597	0.14950166	3	9
GO:0030100	0.00034662	7.37740385	0.96345515	6	58
GO:0034142	0.00040662	9.29864253	0.64784053	5	39
GO:0045766	0.00040662	9.29864253	0.64784053	5	39
GO:0050921	0.00040662	9.29864253	0.64784053	5	39
GO:0001776	0.00040758	13.8922559	0.3654485	4	22
GO:0002698	0.00040758	13.8922559	0.3654485	4	22
GO:0098542	0.00041031	5.11321948	1.82724252	8	110
GO:0040012	0.00041961	3.62068966	3.92026578	12	236
GO:0001818	0.00045877	9.03076923	0.66445183	5	40
GO:0002920	0.00048466	26.4626866	0.16611296	3	10
GO:0002687	0.00048724	13.1578947	0.3820598	4	23
GO:0045453	0.00048724	13.1578947	0.3820598	4	23
GO:0002758	0.00048807	5.71729958	1.42857143	7	86
GO:1901700	0.00050688	2.80650888	7.85714286	18	473
GO:0007155	0.00051151	2.88215504	7.17607973	17	432
GO:0022610	0.00051151	2.88215504	7.17607973	17	432
GO:0032386	0.00051283	4.04471545	2.89036545	10	174
GO:0034341	0.00051581	8.77777778	0.68106312	5	41
GO:1904018	0.00051581	8.77777778	0.68106312	5	41
GO:0002218	0.00052383	5.64444444	1.44518272	7	87
GO:0050707	0.0005774	12.4969697	0.3986711	4	24
GO:0050730	0.00059368	6.60452586	1.06312292	6	64
GO:0010039	0.00065849	23.1492537	0.18272425	3	11

GO:0030155	0.00067079	3.89607843	2.99003322	10	180
GO:0071621	0.00067882	11.8989899	0.41528239	4	25
GO:0097530	0.00067882	11.8989899	0.41528239	4	25
GO:0070372	0.00070093	6.38125	1.09634551	6	66
GO:0030217	0.00071921	8.09664694	0.73089701	5	44
GO:0048520	0.00071921	8.09664694	0.73089701	5	44
GO:0045765	0.00075989	6.27510246	1.11295681	6	67
GO:0045089	0.0007848	5.24289406	1.5448505	7	93
GO:0042590	0.00079226	11.3553719	0.43189369	4	26
GO:0048661	0.00079226	11.3553719	0.43189369	4	26
GO:0007565	0.00079878	7.89230769	0.74750831	5	45
GO:0002246	0.00080739	121.852941	0.04983389	2	3
GO:0002281	0.00080739	121.852941	0.04983389	2	3
GO:0002438	0.00080739	121.852941	0.04983389	2	3
GO:0002861	0.00080739	121.852941	0.04983389	2	3
GO:0002863	0.00080739	121.852941	0.04983389	2	3
GO:0002864	0.00080739	121.852941	0.04983389	2	3
GO:0002866	0.00080739	121.852941	0.04983389	2	3
GO:0019372	0.00080739	121.852941	0.04983389	2	3
GO:0030853	0.00080739	121.852941	0.04983389	2	3
GO:0030889	0.00080739	121.852941	0.04983389	2	3
GO:0032740	0.00080739	121.852941	0.04983389	2	3
GO:0033004	0.00080739	121.852941	0.04983389	2	3
GO:0090594	0.00080739	121.852941	0.04983389	2	3
GO:2001300	0.00080739	121.852941	0.04983389	2	3
GO:0051241	0.00082033	3.17165215	4.83388704	13	291
GO:0007166	0.00084169	2.36975858	13.4883721	25	812
GO:0030225	0.00086756	20.5721393	0.19933555	3	12
GO:0061082	0.00086756	20.5721393	0.19933555	3	12
GO:0030168	0.00089162	5.12121212	1.57807309	7	95
GO:0042221	0.0009059	2.22709809	19.4186047	32	1169
GO:0048585	0.00090997	2.89304813	6.17940199	15	372
GO:0008284	0.00093066	3.47521889	3.68770764	11	222
GO:0070371	0.00096007	5.9765625	1.1627907	6	70
GO:0002224	0.00097744	7.51282051	0.7807309	5	47
GO:0050870	0.00097744	7.51282051	0.7807309	5	47
GO:1901342	0.00103511	5.88317308	1.17940199	6	71
GO:0007259	0.00105821	10.4040404	0.46511628	4	28
GO:0034101	0.00105821	10.4040404	0.46511628	4	28
GO:0032722	0.00111445	18.5104478	0.21594684	3	13
GO:0032755	0.00111445	18.5104478	0.21594684	3	13
GO:0032760	0.00111445	18.5104478	0.21594684	3	13
GO:0060443	0.00111445	18.5104478	0.21594684	3	13

GO:1903557	0.00111445	18.5104478	0.21594684	3	13
GO:0032879	0.00113711	2.33816425	12.9568106	24	780
GO:0034112	0.00118427	7.16783217	0.81395349	5	49
GO:1903039	0.00118427	7.16783217	0.81395349	5	49
GO:0006935	0.00119731	3.03097399	5.03322259	13	303
GO:0042330	0.00119731	3.03097399	5.03322259	13	303
GO:0048771	0.00129907	7.00683761	0.83056478	5	50
GO:0002526	0.00138138	9.5990676	0.49833887	4	30
GO:0022408	0.00138138	9.5990676	0.49833887	4	30
GO:0045619	0.00138138	9.5990676	0.49833887	4	30
GO:0017157	0.00138138	5.53668478	1.24584718	6	75
GO:0050795	0.00138138	5.53668478	1.24584718	6	75
GO:0002762	0.00140157	16.8236092	0.23255814	3	14
GO:0002221	0.00155311	6.70540098	0.86378738	5	52
GO:0002431	0.00156632	9.24130191	0.51495017	4	31
GO:0034134	0.00156632	9.24130191	0.51495017	4	31
GO:0038094	0.00156632	9.24130191	0.51495017	4	31
GO:0002283	0.00159742	60.9117647	0.06644518	2	4
GO:0002349	0.00159742	60.9117647	0.06644518	2	4
GO:0002441	0.00159742	60.9117647	0.06644518	2	4
GO:0002553	0.00159742	60.9117647	0.06644518	2	4
GO:0006957	0.00159742	60.9117647	0.06644518	2	4
GO:0032627	0.00159742	60.9117647	0.06644518	2	4
GO:0032667	0.00159742	60.9117647	0.06644518	2	4
GO:0032763	0.00159742	60.9117647	0.06644518	2	4
GO:0034122	0.00159742	60.9117647	0.06644518	2	4
GO:0060391	0.00159742	60.9117647	0.06644518	2	4
GO:0070391	0.00159742	60.9117647	0.06644518	2	4
GO:0071223	0.00159742	60.9117647	0.06644518	2	4
GO:0071281	0.00159742	60.9117647	0.06644518	2	4
GO:0071624	0.00159742	60.9117647	0.06644518	2	4
GO:0090023	0.00159742	60.9117647	0.06644518	2	4
GO:1902624	0.00159742	60.9117647	0.06644518	2	4
GO:0045124	0.0017312	15.4179104	0.24916944	3	15
GO:0050715	0.0017312	15.4179104	0.24916944	3	15
GO:0002474	0.00176785	8.90909091	0.53156146	4	32
GO:0050663	0.00176785	8.90909091	0.53156146	4	32
GO:1903532	0.00181007	5.22816781	1.31229236	6	79
GO:1903530	0.00182478	3.37521368	3.40531561	10	205
GO:1901701	0.00197276	2.85050574	5.31561462	13	320
GO:0048660	0.00198671	8.59979101	0.54817276	4	33
GO:0008283	0.00208097	2.43920836	8.8538206	18	533
GO:0002260	0.00210547	14.228473	0.26578073	3	16

GO:0050764	0.00210547	14.228473	0.26578073	3	16
GO:0044706	0.00216852	6.173454	0.93023256	5	56
GO:0052548	0.00219287	5.01809211	1.36212625	6	82
GO:0001525	0.0022008	3.86133847	2.35880399	8	142
GO:0001894	0.00234676	6.05325444	0.94684385	5	57
GO:0007162	0.00234676	6.05325444	0.94684385	5	57
GO:0048659	0.00247944	8.04105572	0.58139535	4	35
GO:0032642	0.00252638	13.2089552	0.28239203	3	17
GO:2000106	0.00252638	13.2089552	0.28239203	3	17
GO:0001774	0.00263378	40.5980392	0.08305648	2	5
GO:0002639	0.00263378	40.5980392	0.08305648	2	5
GO:0002675	0.00263378	40.5980392	0.08305648	2	5
GO:0015684	0.00263378	40.5980392	0.08305648	2	5
GO:0032660	0.00263378	40.5980392	0.08305648	2	5
GO:0045577	0.00263378	40.5980392	0.08305648	2	5
GO:0045779	0.00263378	40.5980392	0.08305648	2	5
GO:0050855	0.00263378	40.5980392	0.08305648	2	5
GO:0060397	0.00263378	40.5980392	0.08305648	2	5
GO:0060341	0.00274862	2.63579387	6.19601329	14	373
GO:0071345	0.00274899	3.40716737	3.00664452	9	181
GO:0071346	0.00275478	7.78787879	0.59800664	4	36
GO:1902107	0.00275478	7.78787879	0.59800664	4	36
GO:0022603	0.00280194	2.84427537	4.86710963	12	293
GO:1902533	0.00288272	2.83345561	4.88372093	12	294
GO:0006915	0.00290358	2.35528031	9.11960133	18	549
GO:0052547	0.0029632	4.7025463	1.44518272	6	87
GO:0002088	0.0029958	12.3253731	0.29900332	3	18
GO:0019369	0.0029958	12.3253731	0.29900332	3	18
GO:0046456	0.0029958	12.3253731	0.29900332	3	18
GO:1901570	0.0029958	12.3253731	0.29900332	3	18
GO:0002576	0.0030504	7.55004591	0.61461794	4	37
GO:1903036	0.0030504	7.55004591	0.61461794	4	37
GO:0051047	0.00313892	4.64405488	1.46179402	6	88
GO:0022409	0.00316779	5.61538462	1.01328904	5	61
GO:0051046	0.00318088	3.10663507	3.67109635	10	221
GO:0007165	0.00318927	1.98938832	26.3621262	38	1587
GO:0012501	0.00321123	2.33008037	9.20265781	18	554
GO:2000026	0.00334633	2.36994882	8.48837209	17	511
GO:0030336	0.00340184	5.51551957	1.02990033	5	62
GO:0048002	0.00340184	5.51551957	1.02990033	5	62
GO:0023056	0.00351236	2.41419344	7.79069767	16	469
GO:0032602	0.00351547	11.5522388	0.31561462	3	19
GO:0032680	0.00351547	11.5522388	0.31561462	3	19

GO:0046850	0.00351547	11.5522388	0.31561462	3	19
GO:0060389	0.00351547	11.5522388	0.31561462	3	19
GO:1903555	0.00351547	11.5522388	0.31561462	3	19
GO:0009743	0.00390696	5.32594524	1.06312292	5	64
GO:0010647	0.0039082	2.38460294	7.87375415	16	474
GO:0001821	0.0039083	30.4411765	0.09966777	2	6
GO:0001913	0.0039083	30.4411765	0.09966777	2	6
GO:0002719	0.0039083	30.4411765	0.09966777	2	6
GO:0030852	0.0039083	30.4411765	0.09966777	2	6
GO:0032620	0.0039083	30.4411765	0.09966777	2	6
GO:0032762	0.0039083	30.4411765	0.09966777	2	6
GO:0033008	0.0039083	30.4411765	0.09966777	2	6
GO:0042119	0.0039083	30.4411765	0.09966777	2	6
GO:0042554	0.0039083	30.4411765	0.09966777	2	6
GO:0043306	0.0039083	30.4411765	0.09966777	2	6
GO:0050832	0.0039083	30.4411765	0.09966777	2	6
GO:0051608	0.0039083	30.4411765	0.09966777	2	6
GO:0060390	0.0039083	30.4411765	0.09966777	2	6
GO:0060396	0.0039083	30.4411765	0.09966777	2	6
GO:0072678	0.0039083	30.4411765	0.09966777	2	6
GO:0050714	0.00406609	6.91582492	0.66445183	4	40
GO:0070374	0.00406609	6.91582492	0.66445183	4	40
GO:0051050	0.00407522	2.8315678	4.43521595	11	267
GO:0032640	0.004087	10.8700615	0.33222591	3	20
GO:0045621	0.004087	10.8700615	0.33222591	3	20
GO:0071706	0.004087	10.8700615	0.33222591	3	20
GO:1902106	0.004087	10.8700615	0.33222591	3	20
GO:0006887	0.00427298	3.43569892	2.62458472	8	158
GO:0050793	0.00434455	2.17791602	11.013289	20	663
GO:1903708	0.0044499	6.72727273	0.68106312	4	41
GO:2000146	0.00446381	5.14880202	1.09634551	5	66
GO:0050729	0.00471188	10.2636816	0.34883721	3	21
GO:0051279	0.00471188	10.2636816	0.34883721	3	21
GO:0051246	0.0048255	2.12315271	11.910299	21	717
GO:0050731	0.00485747	6.54864434	0.69767442	4	42
GO:0042592	0.00493724	2.38028169	7.3255814	15	441
GO:0019882	0.0050752	4.98290598	1.12956811	5	68
GO:0018108	0.00509173	4.17548077	1.61129568	6	97
GO:0018212	0.00535381	4.12907609	1.62790698	6	98
GO:0032388	0.00535381	4.12907609	1.62790698	6	98
GO:0032880	0.00538843	2.71810883	4.6013289	11	277
GO:0006636	0.00539151	9.72113119	0.3654485	3	22
GO:0030512	0.00539151	9.72113119	0.3654485	3	22

GO:0071887	0.00539151	9.72113119	0.3654485	3	22
GO:1903845	0.00539151	9.72113119	0.3654485	3	22
GO:2000177	0.00539151	9.72113119	0.3654485	3	22
GO:0002228	0.00541301	24.3470588	0.11627907	2	7
GO:0002701	0.00541301	24.3470588	0.11627907	2	7
GO:0002720	0.00541301	24.3470588	0.11627907	2	7
GO:0008354	0.00541301	24.3470588	0.11627907	2	7
GO:0009620	0.00541301	24.3470588	0.11627907	2	7
GO:0032733	0.00541301	24.3470588	0.11627907	2	7
GO:0033005	0.00541301	24.3470588	0.11627907	2	7
GO:0034121	0.00541301	24.3470588	0.11627907	2	7
GO:0036230	0.00541301	24.3470588	0.11627907	2	7
GO:0042267	0.00541301	24.3470588	0.11627907	2	7
GO:0043302	0.00541301	24.3470588	0.11627907	2	7
GO:0046851	0.00541301	24.3470588	0.11627907	2	7
GO:0050869	0.00541301	24.3470588	0.11627907	2	7
GO:0071378	0.00541301	24.3470588	0.11627907	2	7
GO:0090022	0.00541301	24.3470588	0.11627907	2	7
GO:1902622	0.00541301	24.3470588	0.11627907	2	7
GO:2000108	0.00541301	24.3470588	0.11627907	2	7
GO:0002768	0.00596882	3.23392169	2.77408638	8	167
GO:0048514	0.00596882	3.23392169	2.77408638	8	167
GO:0045670	0.00612715	9.23283582	0.3820598	3	23
GO:1903725	0.00612715	9.23283582	0.3820598	3	23
GO:0042113	0.00622917	6.06504065	0.74750831	4	45
GO:0009991	0.00628321	2.97189696	3.40531561	9	205
GO:0008219	0.00645664	2.15726943	9.81727575	18	591
GO:0016265	0.00645664	2.15726943	9.81727575	18	591
GO:0051271	0.00647276	4.68082664	1.19601329	5	72
GO:0007154	0.00658156	1.88009788	31.2458472	42	1881
GO:0009967	0.00662045	2.35957179	6.82724252	14	411
GO:0019221	0.00687289	3.45822567	2.25913621	7	136
GO:1903076	0.00691997	8.79104478	0.3986711	3	24
GO:1904375	0.00691997	8.79104478	0.3986711	3	24
GO:0045785	0.00713946	3.87053571	1.72757475	6	104
GO:0051222	0.00713946	3.87053571	1.72757475	6	104
GO:0001910	0.00714012	20.2843137	0.13289037	2	8
GO:0002292	0.00714012	20.2843137	0.13289037	2	8
GO:0002437	0.00714012	20.2843137	0.13289037	2	8
GO:0002637	0.00714012	20.2843137	0.13289037	2	8
GO:0002707	0.00714012	20.2843137	0.13289037	2	8
GO:0010543	0.00714012	20.2843137	0.13289037	2	8
GO:0019370	0.00714012	20.2843137	0.13289037	2	8

GO:0031341	0.00714012	20.2843137	0.13289037	2	8
GO:0034104	0.00714012	20.2843137	0.13289037	2	8
GO:0045730	0.00714012	20.2843137	0.13289037	2	8
GO:2001267	0.00714012	20.2843137	0.13289037	2	8
GO:2001269	0.00714012	20.2843137	0.13289037	2	8
GO:0044700	0.00724788	1.86108595	30.3986711	41	1830
GO:0023052	0.00741343	1.85742891	30.4318937	41	1832
GO:0002479	0.00777104	8.38941655	0.41528239	3	25
GO:0030218	0.00777104	8.38941655	0.41528239	3	25
GO:0051223	0.00803035	2.84956606	3.53820598	9	213
GO:0051130	0.00805477	2.45577211	5.54817276	12	334
GO:0051701	0.00842878	5.52053872	0.81395349	4	49
GO:0097191	0.00857548	4.35042735	1.27906977	5	77
GO:0010033	0.0085846	1.95390925	14.1694352	23	853
GO:0010522	0.00868132	8.02271252	0.43189369	3	26
GO:0030879	0.00868132	8.02271252	0.43189369	3	26
GO:0045638	0.00868132	8.02271252	0.43189369	3	26
GO:0042981	0.00885556	2.27068127	7.05980066	14	425
GO:0032026	0.00908206	17.3823529	0.14950166	2	9
GO:0048662	0.00908206	17.3823529	0.14950166	2	9
GO:0050798	0.00908206	17.3823529	0.14950166	2	9
GO:0050853	0.00908206	17.3823529	0.14950166	2	9
GO:0060603	0.00908206	17.3823529	0.14950166	2	9
GO:0070228	0.00908206	17.3823529	0.14950166	2	9
GO:0090025	0.00908206	17.3823529	0.14950166	2	9
GO:1903307	0.00908206	17.3823529	0.14950166	2	9
GO:0040013	0.00953575	4.23076923	1.31229236	5	79
GO:0060249	0.00953575	4.23076923	1.31229236	5	79
GO:0043067	0.00959445	2.24638554	7.12624585	14	429
GO:1903729	0.00965167	7.68656716	0.44850498	3	27
GO:0023057	0.00966694	2.39122257	5.68106312	12	342
GO:0009968	0.00969583	2.48695091	4.9833887	11	300

Term	Genes	padjust
immune resp	AIF1 APBB1IP	2.19E-18
immune syst	AIF1 APBB1IP	3.68E-15
positive regul	AIF1 B2M C1	1.34E-14
defense resp	AIF1 ALOX5 A	1.08E-13
inflammatory	AIF1 ALOX5 A	5.03E-13
regulation of	AIF1 B2M C1	1.44E-12
leukocyte act	AIF1 APBB1IP	2.75E-12
myeloid leuk	AIF1 CD37 CX	5.82E-12
immune effe	APBB1IP B2M	5.82E-12
leukocyte me	B2M C1QB C1	1.08E-10
cell activatio	AIF1 APBB1IP	1.76E-10
regulation of	B2M C1QB C1	2.08E-10
positive regul	B2M C1QB C1	5.65E-10
regulation of	AIF1 CD37 FC	3.16E-09
tolerance ind	C3 C3AR1 LG	3.16E-09
regulation of	B2M C3 FCER	3.33E-09
innate immu	AIF1 B2M C1	5.88E-09
regulation of	AIF1 CD37 FC	8.75E-09
positive regul	B2M C3 CD3	1.61E-08
response to s	AIF1 ALOX5 A	2.06E-08
lymphocyte a	AIF1 APBB1IP	3.84E-08
negative regu	CD37 HMOX1	3.89E-08
regulation of	C3 FCER1G H	4.96E-08
lymphocyte	B2M C1QB C1	5.50E-08
cell activatio	APBB1IP CX3	5.59E-08
leukocyte act	APBB1IP CX3	5.59E-08
adaptive imm	B2M C1QB C1	7.77E-08
negative regu	INPP5D LGAL	7.77E-08
negative regu	INPP5D LGAL	7.77E-08
humoral imm	B2M C1QB C1	1.10E-07
adaptive imm	B2M C1QB C1	1.31E-07
negative regu	CD37 HMOX1	1.40E-07
activation of	C1QB C1QC C	1.47E-07
myeloid cell	CX3CR1 FCER	1.89E-07
negative regu	INPP5D LGAL	2.09E-07
T cell activati	AIF1 APBB1IP	3.93E-07
T cell aggrega	AIF1 APBB1IP	3.93E-07
lymphocyte a	AIF1 APBB1IP	3.93E-07
leukocyte mi	AIF1 C3AR1 C	5.55E-07
regulation of	AIF1 INPP5D	5.68E-07

lymphocyte p	AIF1 INPP5D	6.25E-07
leukocyte agg	AIF1 APBB1IP	6.55E-07
regulation of	AIF1 INPP5D	6.72E-07
mononuclear	AIF1 INPP5D	7.05E-07
regulation of	B2M C3 CD14	7.85E-07
regulation of	FCER1G HMO	8.47E-07
regulation of	FCER1G HMO	8.47E-07
negative regu	C1QC CD37	8.47E-07
regulation of	AIF1 INPP5D	1.17E-06
leukocyte pro	AIF1 INPP5D	1.28E-06
positive regul	AIF1 B2M C1	1.31E-06
regulation of	FCER1G HMO	1.43E-06
leukocyte cell	AIF1 APBB1IP	1.43E-06
regulation of	B2M C3 C3AR	1.74E-06
regulation of	B2M C3 CD37	2.25E-06
leukocyte diff	B2M C1QC CS	2.51E-06
immunoglobu	C1QB C1QC C	2.51E-06
B cell mediate	C1QB C1QC C	3.43E-06
regulation of	FCER1G HMO	3.57E-06
positive regul	AIF1 FCER1G	3.89E-06
response to b	B2M CD14 CX	4.33E-06
myeloid leuko	C3 FCER1G HI	4.33E-06
negative regu	INPP5D LGALS	4.33E-06
regulation of	AIF1 B2M C3	4.55E-06
positive regul	AIF1 FCER1G	4.83E-06
response to v	AIF1 APBB1IP	4.89E-06
leukocyte che	AIF1 C3AR1 C	4.89E-06
regulation of	FCER1G HMO	4.89E-06
immune syste	B2M C1QC C3	5.34E-06
homotypic ce	AIF1 APBB1IP	5.34E-06
response to s	AIF1 ALOX5 A	6.56E-06
cytokine proc	B2M C3 C3AR	8.88E-06
mast cell acti	FCER1G HMO	1.00E-05
regulation of	B2M C3 FCER	1.00E-05
mast cell deg	FCER1G HMO	1.00E-05
mast cell med	FCER1G HMO	1.43E-05
regulation of	AIF1 ARHGDI	1.91E-05
positive regul	B2M C3 C3AR	1.95E-05
regulation of	AIF1 INPP5D	2.16E-05
lysosome loca	FCER1G HMO	3.54E-05
mast cell acti	FCER1G HMO	3.54E-05
T cell prolifer	AIF1 ITGB2 LG	4.08E-05
dendritic cell	LYN SPI1 TGF	4.29E-05

leukocyte de	FCER1G HMO	4.50E-05
negative regu	HMOX1 INPP	4.50E-05
endocytosis	AIF1 B2M C3	6.04E-05
immune resp	C3AR1 CD14	7.97E-05
hematopoieti	B2M C1QC C	9.09E-05
positive regul	B2M C3 FCER	9.09E-05
regulation of	B2M CSF1R F	9.43E-05
cell chemota	AIF1 C3AR1 C	0.00011506
homeostasis	FCER1G HAM	0.00011613
cellular respo	B2M CD14 C	0.00012806
tolerance ind	LYN TGFB1 T	0.00012806
positive regul	C3 FCER1G T	0.00012806
positive regul	C3 FCER1G T	0.00012806
response to e	B2M CD14 C	0.0001289
response to c	B2M CD14 C	0.0001289
myeloid dend	CD37 SPI1 TG	0.0001289
regulation of	C3 FCER1G P	0.0001289
regulation of	C3 FCER1G P	0.0001289
regulation of	AIF1 LGALS9	0.00013108
regulation of	C3 CX3CR1 F	0.00013485
myeloid leuk	C1QC CSF1R	0.00015169
cell killing	B2M CTSC HA	0.00015472
response to b	B2M CD14 C	0.00016117
cell migration	AIF1 ARHGDI	0.0001701
regulation of	C1QC CSF1R	0.0001871
response to li	AIF1 B2M C3	0.00018849
regulation of	AIF1 LGALS9	0.00020298
cellular respo	B2M CD14 C	0.00020298
myeloid leuk	AIF1 C3AR1 C	0.00020298
humoral imm	C1QB C1QC C	0.00020298
positive regul	B2M C3 FCER	0.00020298
positive regul	AIF1 C3AR1 C	0.00021462
regulated sec	FCER1G HMO	0.00021658
regulation of	C1QC CSF1R	0.00022651
lymphocyte d	B2M FCER1G	0.00024408
hemopoiesis	B2M C1QC C	0.00024472
regulation of	B2M C3 FCER	0.00024791
negative regu	FCER1G HAM	0.00025522
phagocytosis	AIF1 C3 CD14	0.00026242
regulation of	AIF1 LGALS9	0.00026242
positive regul	C3 CD14 FCE	0.00029878
positive regul	B2M C3 FCER	0.00030225
positive regul	B2M C3 FCER	0.00030225

cell motility	AIF1 ARHGDII	0.00032669
localization o	AIF1 ARHGDII	0.00032669
single organis	AIF1 APBB1IP	0.00033492
regulation of	AIF1 LGALS9 I	0.0003454
regulation of	B2M CD37 FC	0.00038434
regulation of	B2M C3 FCER	0.00038434
response to e	AIF1 ALOX5 B	0.00039096
myeloid cell h	FCER1G HAM	0.00039223
negative regu	AIF1 CD37 HN	0.00039777
regulation of	C3 CX3CR1 FC	0.00040553
complement	C1QB C1QC C	0.00042823
negative regu	LGALS9 PTPN	0.00042823
positive regul	AIF1 C3 C3AR	0.00044209
wound healin	APBB1IP C3 F	0.00046952
locomotion	AIF1 ARHGDII	0.00050287
regulation of	AIF1 C3AR1 H	0.00051642
multi-organis	ADAM28 ARH	0.00056149
regulation of	B2M C3 CD14	0.00057753
regulation of	B2M C3 CD14	0.00058565
myeloid cell c	C1QC CSF1R I	0.00067609
response to li	B2M CD14 CX	0.00074947
positive regul	AIF1 C3AR1 C	0.00077096
positive regul	AIF1 C3AR1 C	0.00077096
single organis	AIF1 APBB1IP	0.00077096
cellular respo	B2M CD14 CX	0.00077096
response to n	B2M CD14 CX	0.00079478
positive regul	AIF1 INPP5D I	0.00080899
positive regul	B2M CD37 FC	0.00081077
vesicle-media	AIF1 B2M C3	0.000838
T cell activati	APBB1IP FCEI	0.00107885
production o	ALOX5 FCER1	0.00107885
regulation of	B2M FCER1G	0.00107885
macrophage	AIF1 CX3CR1	0.00107885
protein activa	C1QB C1QC C	0.00107885
regulation of	CD14 FCER1G	0.00112603
regulation of	AIF1 ALOX5 A	0.00113669
positive regul	AIF1 C3AR1 C	0.00128379
regulation of	AIF1 ARHGDII	0.00129293
positive regul	AIF1 ALOX5 A	0.00134047
immune resp	C3AR1 CD14 I	0.00134047
regulation of	AIF1 C3AR1 L	0.00134047
leukocyte me	B2M CTSC LG	0.00138359
defense resp	B2M FCER1G	0.00158006

regulation of	AIF1 LGALS9	0.00180149
response to c	AIF1 B2M CD	0.0020032
regulation of	AIF1 ARHGDI	0.00228452
negative regu	LGALS9 PTPN	0.00228452
positive regul	C3 FCER1G V	0.00232476
positive regul	C3 C3AR1 TG	0.00232476
myeloid dend	SPI1 TGFB1 T	0.00232476
regulation of	APBB1IP C3 F	0.00232476
lymphocyte a	APBB1IP FCE	0.00243369
production o	B2M CD37 FC	0.00243369
cell-cell adhe	AIF1 APBB1IP	0.00246604
regulation of	AIF1 ARHGDI	0.00255497
cellular respo	AIF1 ALOX5A	0.00269665
cytokine proc	B2M FCER1G	0.00271042
regulation of	FCER1G INPP	0.00271042
negative regu	LGALS9 PTPN	0.00271042
positive regul	B2M C3 CD14	0.00271042
bone remode	CSF1R HAMP	0.00271042
blood coagul	APBB1IP C3 F	0.00275332
hemostasis	APBB1IP C3 F	0.00299843
coagulation	APBB1IP C3 F	0.00299843
interleukin-6	FCER1G INPP	0.00328627
receptor-mec	B2M CD14 C	0.00330227
complement	C1QB C1QC C	0.00334222
regulation of	C3 C3AR1 TG	0.00334222
immune resp	C3AR1 FCER1	0.0035721
type IIa hype	C3 FCER1G	0.0035721
regulation of	C3 FCER1G	0.0035721
positive regul	C3 FCER1G	0.0035721
type II hypers	C3 FCER1G	0.0035721
hypersensitiv	C3 FCER1G	0.0035721
regulation of	C3 FCER1G	0.0035721
positive regul	C3 FCER1G	0.0035721
negative regu	HMOX1 LGAL	0.0035721
regulation of	C3 FCER1G	0.0035721
positive regul	C3 FCER1G	0.0035721
common-par	TGFB1 TGFBR	0.0035721
muscle hyper	AIF1 HMOX1	0.0035721
negative regu	HMOX1 LGAL	0.0035721
regulation of	B2M HAMP	0.0035721
negative regu	HMOX1 LGAL	0.0035721
negative regu	HMOX1 LGAL	0.0035721
regulatory T	LGALS9 TGFB	0.0035721

negative regu	HMOX1 LGAL	0.0035721
movement of	AIF1 ARHGDI	0.0035721
regulation of	C1QC CSF1R I	0.00358708
regulation of	INPP5D LYN F	0.00358708
cellular respo	AIF1 ALOX5A	0.00360448
regulation of	C1QC CSF1R I	0.00364775
regulation of	AIF1 C3AR1 L	0.00364775
regulation of	AIF1 C3AR1 C	0.00404126
positive regul	AIF1 ALOX5 B	0.00414231
positive regul	AIF1 C3AR1 L	0.00414231
neutrophil ch	C3AR1 FCER1	0.00414231
regulation of	CSF1R HAMP	0.00414231
negative regu	LGALS9 PTPN	0.00414231
neutrophil mi	C3AR1 FCER1	0.00414231
negative regu	HMOX1 LGAL	0.00414231
vascular endo	C3 C3AR1 TG	0.00414231
granulocyte c	C1QC INPP5D	0.00414231
response to s	TGFB1 TGFBR	0.00414231
regulation of	INPP5D LYN S	0.00414231
response to c	TGFB1 TGFBR	0.00414231
regulation of	B2M C3 CD14	0.00416387
toll-like recep	CD14 ITGB2 L	0.00479335
positive regul	C3 C3AR1 CX	0.00479335
positive regul	AIF1 C3AR1 L	0.00479335
leukocyte hor	FCER1G LGAL	0.00479335
negative regu	HMOX1 LGAL	0.00479335
defense respo	B2M CD37 FC	0.00480531
regulation of	AIF1 ARHGDI	0.00489371
negative regu	HMOX1 INPP	0.00532823
regulation of	C3 CD37 PTP	0.00557592
positive regul	AIF1 C3AR1 L	0.00557592
bone resorpti	CSF1R HAMP	0.00557592
innate immur	CD14 FCER1G	0.00557592
response to c	AIF1 B2M C3	0.00575202
cell adhesion	AIF1 APBB1IP	0.00575202
biological ad	AIF1 APBB1IP	0.00575202
regulation of	FCER1G HMO	0.00575202
response to i	AIF1 B2M CX	0.00575202
positive regul	C3 C3AR1 CX	0.00575202
activation of i	CD14 FCER1G	0.00581829
regulation of	CD14 CSF1R L	0.00638792
regulation of	CSF1R ITGB2	0.00654218
response to i	B2M HAMP H	0.00722788

regulation of	AIF1 APBB1IP	0.00733412
granulocyte c	C3AR1 FCER1	0.00736442
granulocyte n	C3AR1 FCER1	0.00736442
regulation of	C3 CSF1R LG	0.0075749
T cell differen	B2M FCER1G	0.00771294
positive regul	AIF1 C3AR1 L	0.00771294
regulation of	C3 C3AR1 CX	0.00807101
positive regul	CD14 FCER1G	0.00807101
antigen proce	B2M CYBB FC	0.00807101
positive regul	AIF1 C3AR1 H	0.00807101
female pregn	ARHGDIB LG	0.00807101
wound healin	HMOX1 TGFB	0.00807101
macrophage	CX3CR1 TYRO	0.00807101
acute inflam	C3 FCER1G	0.00807101
regulation of	C3 FCER1G	0.00807101
positive regul	C3 FCER1G	0.00807101
regulation of	C3 FCER1G	0.00807101
positive regul	C3 FCER1G	0.00807101
lipoxygenase	ALOX5 ALOX	0.00807101
negative regu	C1QC INPP5D	0.00807101
negative regu	INPP5D LYN	0.00807101
positive regul	MYD88 TGFB	0.00807101
negative regu	HMOX1 LGAL	0.00807101
inflammatory	HMOX1 TGFB	0.00807101
lipoxin metab	ALOX5 ALOX	0.00807101
negative regu	ARHGDIB C1	0.00817123
cell surface r	B2M C3AR1	0.00835426
macrophage	C1QC CSF1R	0.00855035
myeloid leuk	FCER1G HMO	0.00855035
platelet activ	APBB1IP FCE	0.00875666
response to c	AIF1 ALOX5 A	0.00886583
negative regu	AIF1 CX3CR1	0.00887461
positive regul	AIF1 C3AR1 C	0.00904487
ERK1 and ER	C3 CSF1R LG	0.00929841
toll-like recep	CD14 ITGB2 L	0.00940155
positive regul	AIF1 LGALS9	0.00940155
regulation of	C3 C3AR1 CX	0.00992214
JAK-STAT cas	CSF1R HAMP	0.01007463
erythrocyte h	HMOX1 INPP	0.01007463
positive regul	CSF1R HMOX	0.01043255
positive regul	FCER1G LGAL	0.01043255
positive regul	CD14 FCER1G	0.01043255
mammary gla	CSF1R TGFB1	0.01043255

positive regul	CD14 FCER1G	0.01043255
regulation of	AIF1 ARHGDI	0.01060925
positive regul	AIF1 LGALS9	0.01097604
positive regul	AIF1 LGALS9	0.01097604
chemotaxis	AIF1 C3AR1 C	0.01102393
taxis	AIF1 C3AR1 C	0.01102393
tissue remod	CSF1R HAMP	0.0119216
acute inflam	ALOX5 C3 FC	0.01247252
negative regu	LGALS9 PTPN	0.01247252
regulation of	INPP5D LGAL	0.01247252
regulation of	FCER1G HMO	0.01247252
regulation of	AIF1 C3AR1 L	0.01247252
negative regu	C1QC INPP5D	0.01261409
pattern recog	CD14 ITGB2 L	0.01350808
Fc receptor m	FCER1G FCGR	0.01350808
toll-like recep	CD14 LYN MY	0.01350808
Fc-gamma re	FCER1G FCGR	0.01350808
neutrophil ac	FCER1G TYRO	0.01350808
histamine pro	LYN VAMP8	0.01350808
histamine sec	LYN VAMP8	0.01350808
histamine sec	LYN VAMP8	0.01350808
complement	C3 VSIG4	0.01350808
interleukin-2	MYD88 TGFB	0.01350808
regulation of	MYD88 TGFB	0.01350808
regulation of	FCER1G HMO	0.01350808
negative regu	LYN PIK3AP1	0.01350808
positive regul	TGFB1 TGFBR	0.01350808
response to li	CD14 TREM2	0.01350808
cellular respo	CD14 TREM2	0.01350808
cellular respo	B2M HMOX1	0.01350808
positive regul	C3AR1 RAC2	0.01350808
positive regul	C3AR1 RAC2	0.01350808
positive regul	C3AR1 RAC2	0.01350808
regulation of	CSF1R HAMP	0.0145514
positive regul	CD14 CSF1R L	0.0145514
antigen proce	B2M CYBB FC	0.01477076
cytokine secr	CD14 CSF1R L	0.01477076
positive regul	CD14 CSF1R F	0.01507854
regulation of	CD14 CSF1R F	0.01515594
cellular respo	AIF1 B2M CD	0.01633654
regulation of	AIF1 C3AR1 H	0.01640355
cell proliferat	AIF1 C3AR1 C	0.01713126
lymphocyte h	LGALS9 LYN T	0.0172316

regulation of	C3 FCER1G T	0.0172316
multi-multice	ARHGDIB LG	0.01769591
regulation of	C3 CD14 CTS	0.01784256
angiogenesis	C3 C3AR1 CX	0.01785522
tissue homeo	B2M CSF1R H	0.01892965
negative regu	ARHGDIB LG	0.01892965
smooth musc	AIF1 C3AR1 H	0.01994238
regulation of	CSF1R HMOX	0.02020385
regulation of	FCER1G LGAL	0.02020385
microglial cel	AIF1 CX3CR1	0.02053466
positive regul	CD37 TGFB1	0.02053466
positive regul	C3 FCER1G	0.02053466
ferrous iron t	B2M HAMP	0.02053466
regulation of	MYD88 TGFB	0.02053466
regulation of	INPP5D PTPN	0.02053466
negative regu	HAMP INPP5	0.02053466
regulation of	LYN PTPN6	0.02053466
JAK-STAT cas	LYN PTPN6	0.02053466
regulation of	CD14 CSF1R	0.02124138
cellular respo	AIF1 B2M CS	0.02124138
cellular respo	AIF1 B2M LG	0.02124138
positive regul	CSF1R INPP5	0.02124138
regulation of	C3 C3AR1 CD	0.0215457
positive regul	C3 CSF1R HM	0.02210615
apoptotic pro	AIF1 CD14 CT	0.02220523
regulation of	C3 CD14 CTS	0.02259942
lens develop	TGFB1 TGFBR	0.02260177
arachidonic a	ALOX5 ALOX	0.02260177
icosanoid bio	ALOX5 ALOX	0.02260177
fatty acid der	ALOX5 ALOX	0.02260177
platelet degr	FCER1G LYN	0.02289028
positive regul	C3 FCER1G T	0.02289028
positive regul	CD14 CSF1R	0.02349153
positive regul	AIF1 LGALS9	0.02364442
regulation of	CD14 CSF1R	0.02367843
signal transd	AIF1 APBB1IP	0.02367843
programmed	AIF1 CD14 CT	0.0237784
regulation of	ARHGDIB C1	0.0247134
negative regu	AIF1 ARHGDI	0.02499148
antigen proc	B2M CYBB FC	0.02499148
positive regul	C3 CD14 CSF1	0.02542585
chemokine p	CSF1R HMOX	0.02542585
regulation of	CD14 FCER1G	0.02542585

regulation of	CSF1R HAMP	0.02542585
pathway-rest	TGFB1 TGFBR	0.02542585
regulation of	CD14 FCER1G	0.02542585
response to c	LYN SLC2A5 T	0.02707754
positive regul	C3 CD14 CSF1	0.02707754
histamine sec	LYN VAMP8	0.02707754
T cell mediat	B2M CTSC	0.02707754
negative regu	HMOX1 TGFB	0.02707754
regulation of	C1QC INPP5D	0.02707754
interleukin-1	MYD88 TGFB	0.02707754
mast cell cyt	FCER1G HMO	0.02707754
positive regul	FCER1G VAM	0.02707754
neutrophil ac	FCER1G TYR	0.02707754
superoxide a	CYBB TGFB1	0.02707754
positive regul	FCER1G VAM	0.02707754
defense resp	HAMP TGFB1	0.02707754
histamine tra	LYN VAMP8	0.02707754
regulation of	TGFB1 TGFBR	0.02707754
growth horm	LYN PTPN6	0.02707754
T cell migrati	AIF1 CXCL16	0.02707754
positive regul	CD14 CSF1R L	0.02783336
positive regul	C3 CSF1R LG	0.02783336
positive regul	B2M C3 CD14	0.02783336
tumor necros	CD14 FCER1G	0.02783336
positive regul	INPP5D LGAL	0.02783336
tumor necros	CD14 FCER1G	0.02783336
negative regu	C1QC INPP5D	0.02783336
exocytosis	FCER1G HMO	0.02902927
regulation of	ARHGDIB C1	0.02944407
positive regul	CSF1R INPP5	0.03008522
negative regu	AIF1 ARHGDI	0.03010653
positive regul	C3 FCER1G V	0.03162725
regulation of	LYN PTPN6 T	0.03162725
regulation of	AIF1 C3 CD14	0.03231236
positive regul	CSF1R LYN T	0.03244882
homeostatic	B2M C3AR1 C	0.03290316
antigen proce	B2M CYBB FC	0.03374227
peptidyl-tyro	CSF1R ITGB2	0.03377192
peptidyl-tyro	CSF1R ITGB2	0.03389486
positive regul	FCER1G LGAL	0.03389486
regulation of	CD14 CSF1R L	0.03389486
unsaturated f	ALOX5 ALOX	0.03389486
negative regu	TGFB1 TGFBR	0.03389486

leukocyte ap	FCER1G LGAL	0.03389486
negative regu	TGFB1 TGFBR	0.03389486
regulation of	CX3CR1 LYN	0.03389486
natural killer	LGALS9 PTPN	0.03389486
negative regu	HMOX1 TGFB	0.03389486
positive regul	B2M FCER1G	0.03389486
germ cell mig	TGFB1 TGFBR	0.03389486
response to	HAMP TGFB1	0.03389486
positive regul	FCER1G LGAL	0.03389486
positive regul	FCER1G VAM	0.03389486
regulation of	LYN PIK3AP1	0.03389486
granulocyte a	FCER1G TYR	0.03389486
natural killer	LGALS9 PTPN	0.03389486
positive regul	FCER1G VAM	0.03389486
negative regu	HAMP INPP5	0.03389486
negative regu	INPP5D LYN	0.03389486
cellular respo	LYN PTPN6	0.03389486
regulation of	C3AR1 RAC2	0.03389486
regulation of	C3AR1 RAC2	0.03389486
positive regul	LGALS9 LYN	0.03389486
immune resp	C3AR1 FCER1	0.03720877
blood vessel	C3 C3AR1 CX	0.03720877
regulation of	CSF1R INPP5	0.03802638
regulation of	IDH1 LYN TG	0.03802638
B cell activat	INPP5D LYN	0.03857397
response to e	AIF1 ALOX5	0.03882276
cell death	AIF1 CD14 CT	0.03971899
death	AIF1 CD14 CT	0.03971899
negative regu	AIF1 ARHGDI	0.0397308
cell communi	AIF1 APBB1IP	0.04031027
positive regul	C3 CD14 CSF1	0.04045992
cytokine-me	B2M CSF1R C	0.04191113
regulation of	TGFB1 TREM	0.0420152
regulation of	TGFB1 TREM	0.0420152
positive regul	AIF1 APBB1IP	0.04207412
positive regul	CD14 CSF1R	0.04207412
regulation of	B2M LGALS9	0.04207412
T cell differen	FCER1G LGAL	0.04207412
inflammatory	C3 FCER1G	0.04207412
regulation of	CD37 TGFB1	0.04207412
negative regu	LGALS9 PTPN	0.04207412
regulation of	FCER1G LYN	0.04207412
leukotriene b	ALOX5 ALOX	0.04207412

regulation of	B2M LGALS9	0.04207412
negative regu	HAMP INPP5	0.04207412
respiratory b	CYBB RAC2	0.04207412
regulation of	CD14 LGALS9	0.04207412
positive regul	CD14 LGALS9	0.04207412
single organis	AIF1 APBB1IP	0.04261933
signaling	AIF1 APBB1IP	0.04350145
antigen proce	B2M CYBB PS	0.04540948
erythrocyte d	INPP5D LYN S	0.04540948
regulation of	CD14 CSF1R L	0.04682695
positive regul	B2M C3 CD14	0.0468717
interaction w	CYBB LGALS9	0.04894638
extrinsic apo	CD14 CX3CR1	0.04964524
response to c	AIF1 B2M C3	0.04964524
regulation of	LYN PTPN6 T	0.04989529
mammary gla	CSF1R TGFB1	0.04989529
negative regu	C1QC INPP5D	0.04989529
regulation of	AIF1 CD14 CT	0.05079246
response to n	C3 CD14	0.05125139
negative regu	AIF1 HMOX1	0.05125139
activated T ce	ITGB2 LGALS	0.05125139
B cell recepto	LYN PTPN6	0.05125139
mammary gla	CSF1R TGFB1	0.05125139
regulation of	LGALS9 LYN	0.05125139
regulation of	AIF1 LYN	0.05125139
positive regul	FCER1G VAM	0.05125139
negative regu	AIF1 ARHGDI	0.05359549
anatomical st	B2M CSF1R H	0.05359549
regulation of	AIF1 CD14 CT	0.05381736
regulation of	TGFB1 TREM	0.05400751
negative regu	CX3CR1 HMO	0.05400751
negative regu	CX3CR1 HMO	0.05406101

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0043435	1.24E-07	Inf	0.01566208	3	3
GO:0071376	1.24E-07	Inf	0.01566208	3	3
GO:0045444	1.08E-05	22.1229947	0.31324158	5	60
GO:0007612	1.73E-05	19.9180328	0.34456573	5	66
GO:0006979	1.80E-05	14.1805556	0.59515899	6	114
GO:1990441	2.60E-05	Inf	0.01044139	2	2
GO:0009891	3.00E-05	7.23441109	2.31276697	10	443
GO:0044708	3.14E-05	10.2820513	0.98671096	7	189
GO:0009612	3.25E-05	17.3193277	0.39155197	5	75
GO:0051173	3.66E-05	7.05229496	2.3649739	10	453
GO:0006352	3.69E-05	16.8300654	0.40199336	5	77
GO:0014070	4.36E-05	8.36673774	1.44091125	8	276
GO:0009893	4.89E-05	5.96398528	5.03796868	14	965
GO:0051254	5.20E-05	7.30260648	1.94209777	9	372
GO:0043401	5.40E-05	55	0.07831039	3	15
GO:0046683	9.33E-05	20.9494949	0.25059326	4	48
GO:0071495	9.44E-05	6.711146	2.09349786	9	401
GO:0010557	9.62E-05	6.69230769	2.09871856	9	402
GO:0010604	9.76E-05	5.6627558	3.88941623	12	745
GO:0010035	0.00011049	10.035596	0.81964879	6	157
GO:0071277	0.00013298	38.7770898	0.10441386	3	20
GO:0014074	0.000138	18.7891156	0.27669673	4	53
GO:0031325	0.00013998	5.41894737	4.03037494	12	772
GO:0045935	0.00015446	6.25064409	2.22923588	9	427
GO:0046697	0.00015515	209.5	0.02088277	2	4
GO:0061469	0.00015515	209.5	0.02088277	2	4
GO:0097201	0.00015515	209.5	0.02088277	2	4
GO:0010243	0.0001566	6.86779059	1.72282867	8	330
GO:0006357	0.0001573	6.2340738	2.23445657	9	428
GO:0009719	0.00015756	5.80798479	2.79829141	10	536
GO:0000302	0.00015963	18.043573	0.28713811	4	55
GO:0033993	0.00016121	7.78762307	1.27384907	7	244
GO:0010628	0.0001661	6.18483412	2.25011865	9	431
GO:0034599	0.00017132	17.6923077	0.2923588	4	56
GO:0007178	0.00017155	11.9132207	0.55339345	5	106
GO:0045944	0.00017857	7.65062241	1.29473185	7	248
GO:0043524	0.00018361	17.3542977	0.2975795	4	57
GO:0031328	0.00018494	6.08842559	2.28144281	9	437
GO:0007179	0.00019654	17.0288066	0.30280019	4	58

GO:0009725	0.00020546	6.57910448	1.79069767	8	343
GO:1901698	0.00023196	6.45328865	1.82202183	8	349
GO:0007611	0.00023201	11.1220044	0.5899383	5	113
GO:0045893	0.00025615	6.35177539	1.8481253	8	354
GO:1903508	0.00025615	6.35177539	1.8481253	8	354
GO:0009628	0.0002824	6.25315425	1.87422876	8	359
GO:1902680	0.0002824	6.25315425	1.87422876	8	359
GO:1901215	0.00028832	15.3037037	0.33412435	4	64
GO:0006366	0.00029373	5.68605241	2.42240152	9	464
GO:0048522	0.00029513	4.91913747	6.7190318	15	1287
GO:0009755	0.00029718	28.6201373	0.13573802	3	26
GO:0034614	0.00029718	28.6201373	0.13573802	3	26
GO:0048661	0.00029718	28.6201373	0.13573802	3	26
GO:0071559	0.00032481	14.8028674	0.34456573	4	66
GO:0071560	0.00032481	14.8028674	0.34456573	4	66
GO:1901700	0.00034025	5.56233422	2.46938776	9	473
GO:0006367	0.00036451	14.3333333	0.35500712	4	68
GO:0036474	0.00038543	104.7	0.03132416	2	6
GO:1901032	0.00038543	104.7	0.03132416	2	6
GO:1903205	0.00038543	104.7	0.03132416	2	6
GO:1903206	0.00038543	104.7	0.03132416	2	6
GO:0007610	0.00043295	6.54504182	1.49311818	7	286
GO:0050890	0.00044647	9.56941176	0.67869008	5	130
GO:0042542	0.00045782	24.3567251	0.15662079	3	30
GO:0009888	0.00048066	5.27920228	2.584243	9	495
GO:0001893	0.00053789	83.74	0.03654485	2	7
GO:0044342	0.00053789	83.74	0.03654485	2	7
GO:0048660	0.00060902	21.9052632	0.17228287	3	33
GO:0032496	0.00064755	12.1985185	0.41243474	4	79
GO:0048545	0.00064941	8.7716263	0.7361177	5	141
GO:0002237	0.00067929	12.0350877	0.41765543	4	80
GO:0043523	0.00067929	12.0350877	0.41765543	4	80
GO:0034248	0.00071212	11.8759019	0.42287613	4	81
GO:0048659	0.00072565	20.5263158	0.18272425	3	35
GO:0008284	0.00073109	6.90277778	1.15899383	6	222
GO:0033554	0.00075837	4.92114269	2.74608448	9	526
GO:0042127	0.00076226	5.31414531	2.16658757	8	415
GO:0035994	0.00091628	59.7857143	0.04698624	2	9
GO:0045932	0.00091628	59.7857143	0.04698624	2	9
GO:0045933	0.00091628	59.7857143	0.04698624	2	9
GO:0045986	0.00091628	59.7857143	0.04698624	2	9
GO:1900408	0.00091628	59.7857143	0.04698624	2	9
GO:1902883	0.00091628	59.7857143	0.04698624	2	9

GO:1903202	0.00091628	59.7857143	0.04698624	2	9
GO:0051591	0.00092586	18.7533835	0.19838633	3	38
GO:0051402	0.00093328	11.0013387	0.45420028	4	87
GO:0070887	0.00102371	4.28625473	4.19743711	11	804
GO:0009889	0.00104759	4.17435897	4.9492169	12	948
GO:0032870	0.0010567	6.40086207	1.24252492	6	238
GO:0045834	0.001243	16.8137652	0.2192691	3	42
GO:1901214	0.00124818	10.1283951	0.49074514	4	94
GO:0033687	0.00139103	46.4777778	0.05742762	2	11
GO:0060716	0.00139103	46.4777778	0.05742762	2	11
GO:1901031	0.00139103	46.4777778	0.05742762	2	11
GO:0048514	0.00140042	7.31663036	0.87185572	5	167
GO:0001890	0.00142432	15.9858793	0.22971049	3	44
GO:0010941	0.00142966	4.7755102	2.38063598	8	456
GO:0048523	0.00148199	3.94266509	5.93592786	13	1137
GO:0051726	0.00148534	5.96370968	1.326056	6	254
GO:0007565	0.0015209	15.6015038	0.23493118	3	45
GO:0071383	0.00162152	15.2350061	0.24015187	3	46
GO:0010611	0.00166396	41.82	0.06264832	2	12
GO:0045923	0.00166396	41.82	0.06264832	2	12
GO:0050873	0.00166396	41.82	0.06264832	2	12
GO:1903201	0.00166396	41.82	0.06264832	2	12
GO:0010033	0.00171243	3.97862233	4.45325107	11	853
GO:0050679	0.00172623	14.8851675	0.24537257	3	47
GO:0008219	0.00178354	4.29421094	3.08542952	9	591
GO:0016265	0.00178354	4.29421094	3.08542952	9	591
GO:0051592	0.00183509	14.5508772	0.25059326	3	48
GO:0009617	0.00188389	9.00110011	0.54817276	4	105
GO:0070997	0.00188389	9.00110011	0.54817276	4	105
GO:0048583	0.00193449	3.8304	5.28334124	12	1012
GO:0042221	0.00195952	3.79354095	6.10299003	13	1169
GO:0002042	0.00196029	38.0090909	0.06786901	2	13
GO:0014743	0.00196029	38.0090909	0.06786901	2	13
GO:0048518	0.00201389	3.86172651	7.88846701	15	1511
GO:0000122	0.00210584	6.63251818	0.95538681	5	183
GO:0010556	0.00210945	3.85747393	4.56288562	11	874
GO:0038095	0.0021625	8.64973545	0.56905553	4	109
GO:0048869	0.00220682	3.7308642	6.17607973	13	1183
GO:0060674	0.00227979	34.8333333	0.0730897	2	14
GO:0070301	0.00227979	34.8333333	0.0730897	2	14
GO:0080134	0.00236645	4.77801609	1.98386331	7	380
GO:0060548	0.00236659	5.40441176	1.45135263	6	278
GO:0001568	0.00260251	6.29915068	1.00237304	5	192

GO:0036473	0.00262222	32.1461538	0.07831039	2	15
GO:0060135	0.00262222	32.1461538	0.07831039	2	15
GO:0033002	0.00271837	12.5708502	0.28713811	3	55
GO:0071248	0.00271837	12.5708502	0.28713811	3	55
GO:0044706	0.00286255	12.3306852	0.2923588	3	56
GO:0010038	0.00289189	7.94931774	0.61604177	4	118
GO:0002763	0.00298736	29.8428571	0.08353109	2	16
GO:0060395	0.00298736	29.8428571	0.08353109	2	16
GO:1900407	0.00298736	29.8428571	0.08353109	2	16
GO:0001944	0.00304453	6.06124924	1.03891789	5	199
GO:0048519	0.00316586	3.54329123	6.40579022	13	1227
GO:0006950	0.00325322	3.55014164	5.59136213	12	1071
GO:0071363	0.00336762	5.00856164	1.55576649	6	298
GO:0006940	0.00337499	27.8466667	0.08875178	2	17
GO:0002573	0.00365425	11.2540835	0.31846227	3	61
GO:0070848	0.00366167	4.91792929	1.58186996	6	303
GO:0031326	0.00372509	3.53679654	4.88134789	11	935
GO:0071407	0.00377575	7.35140018	0.663028	4	127
GO:0035914	0.00378488	26.1	0.09397247	2	18
GO:1902882	0.00378488	26.1	0.09397247	2	18
GO:0071241	0.0038271	11.0606601	0.32368296	3	62
GO:0008283	0.00392046	3.99129252	2.78262933	8	533
GO:0051240	0.00403044	4.30471545	2.17702895	7	417
GO:0071310	0.00420434	3.71826046	3.48220218	9	667
GO:0003300	0.00421682	24.5588235	0.09919317	2	19
GO:0046889	0.00421682	24.5588235	0.09919317	2	19
GO:0009314	0.00433905	7.05555556	0.68913147	4	132
GO:0038093	0.00433905	7.05555556	0.68913147	4	132
GO:0030154	0.00445228	3.38559708	5.78974846	12	1109
GO:0007166	0.00454429	3.52244389	4.23920266	10	812
GO:0014896	0.00467058	23.1888889	0.10441386	2	20
GO:0014897	0.00467058	23.1888889	0.10441386	2	20
GO:0043502	0.00467058	23.1888889	0.10441386	2	20
GO:1901701	0.00480839	4.63136943	1.67062174	6	320
GO:0009059	0.00486155	3.3400722	5.84717608	12	1120
GO:0045639	0.00514595	21.9631579	0.10963455	2	21
GO:0060711	0.00514595	21.9631579	0.10963455	2	21
GO:0051171	0.00521814	3.35306334	5.08495491	11	974
GO:0002041	0.00522069	Inf	0.00522069	1	1
GO:0009444	0.00522069	Inf	0.00522069	1	1
GO:0021538	0.00522069	Inf	0.00522069	1	1
GO:0021940	0.00522069	Inf	0.00522069	1	1
GO:0021986	0.00522069	Inf	0.00522069	1	1

GO:0032056	0.00522069	Inf	0.00522069	1	1
GO:0032058	0.00522069	Inf	0.00522069	1	1
GO:0035633	0.00522069	Inf	0.00522069	1	1
GO:0036066	0.00522069	Inf	0.00522069	1	1
GO:0036476	0.00522069	Inf	0.00522069	1	1
GO:0036497	0.00522069	Inf	0.00522069	1	1
GO:0038097	0.00522069	Inf	0.00522069	1	1
GO:0045341	0.00522069	Inf	0.00522069	1	1
GO:0045343	0.00522069	Inf	0.00522069	1	1
GO:0045345	0.00522069	Inf	0.00522069	1	1
GO:0051132	0.00522069	Inf	0.00522069	1	1
GO:0051133	0.00522069	Inf	0.00522069	1	1
GO:0051135	0.00522069	Inf	0.00522069	1	1
GO:0051866	0.00522069	Inf	0.00522069	1	1
GO:0060005	0.00522069	Inf	0.00522069	1	1
GO:0060734	0.00522069	Inf	0.00522069	1	1
GO:0090360	0.00522069	Inf	0.00522069	1	1
GO:0090361	0.00522069	Inf	0.00522069	1	1
GO:0090362	0.00522069	Inf	0.00522069	1	1
GO:1903207	0.00522069	Inf	0.00522069	1	1
GO:1903208	0.00522069	Inf	0.00522069	1	1
GO:1903898	0.00522069	Inf	0.00522069	1	1
GO:1903916	0.00522069	Inf	0.00522069	1	1
GO:1903917	0.00522069	Inf	0.00522069	1	1
GO:0050877	0.00535162	4.52219626	1.70716659	6	327
GO:0090257	0.00539151	9.72113119	0.3654485	3	70
GO:0001525	0.00563251	6.52818035	0.7413384	4	142
GO:0097285	0.00563251	6.52818035	0.7413384	4	142
GO:0043618	0.0056427	20.86	0.11485524	2	22
GO:2000177	0.0056427	20.86	0.11485524	2	22
GO:0048584	0.005774	3.7137746	2.96013289	8	567
GO:0030522	0.00583456	9.43478261	0.37588989	3	72
GO:0042493	0.00591922	6.43174603	0.75177978	4	144
GO:0007049	0.0059505	3.97939394	2.33364974	7	447
GO:0048646	0.00602725	4.4031155	1.74893213	6	335
GO:0006417	0.00606409	9.29774436	0.38111058	3	73
GO:0002040	0.00616062	19.8619048	0.12007594	2	23
GO:2000112	0.0065174	3.31551861	4.44803037	10	852
GO:0043500	0.00669951	18.9545455	0.12529663	2	24
GO:0043620	0.00669951	18.9545455	0.12529663	2	24
GO:0048513	0.00674782	3.29590229	4.46891315	10	856
GO:0043603	0.00704688	4.9081658	1.26340769	5	242
GO:0001938	0.00725913	18.126087	0.13051732	2	25

GO:0034250	0.00725913	18.126087	0.13051732	2	25
GO:0043534	0.00725913	18.126087	0.13051732	2	25
GO:0009266	0.00729316	8.66736842	0.40721405	3	78
GO:0071496	0.00750105	5.98814815	0.80398671	4	154
GO:0060255	0.00769175	3.09802451	7.02705268	13	1346
GO:0009605	0.00800867	3.3161921	3.82676792	9	733
GO:0034146	0.00843978	16.668	0.14095871	2	27
GO:0034166	0.00843978	16.668	0.14095871	2	27
GO:0051716	0.00864472	3.22925457	9.98196488	16	1912
GO:0043066	0.0087715	4.63764706	1.3312767	5	255
GO:0035666	0.00906039	16.0230769	0.1461794	2	28
GO:0050678	0.00924757	7.9139923	0.4437589	3	85
GO:0043069	0.00935712	4.55998147	1.35215947	5	259
GO:0051094	0.00962547	3.95557851	1.92643569	6	369
GO:0002756	0.0097009	15.4259259	0.15140009	2	29
GO:0007631	0.0097009	15.4259259	0.15140009	2	29
GO:0034162	0.0097009	15.4259259	0.15140009	2	29
GO:0038123	0.0097009	15.4259259	0.15140009	2	29
GO:0038124	0.0097009	15.4259259	0.15140009	2	29
GO:0002768	0.00994892	5.49284254	0.87185572	4	167

Term
response to corticotropin-releasing hormone
cellular response to corticotropin-releasing hormone stimulus
fat cell differentiation
learning
response to oxidative stress
negative regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticul
positive regulation of biosynthetic process
single-organism behavior
response to mechanical stimulus
positive regulation of nitrogen compound metabolic process
DNA-templated transcription, initiation
response to organic cyclic compound
positive regulation of metabolic process
positive regulation of RNA metabolic process
steroid hormone mediated signaling pathway
response to organophosphorus
cellular response to endogenous stimulus
positive regulation of macromolecule biosynthetic process
positive regulation of macromolecule metabolic process
response to inorganic substance
cellular response to calcium ion
response to purine-containing compound
positive regulation of cellular metabolic process
positive regulation of nucleobase-containing compound metabolic process
decidualization
regulation of type B pancreatic cell proliferation
negative regulation of transcription from RNA polymerase II promoter in response to stress
response to organonitrogen compound
regulation of transcription from RNA polymerase II promoter
response to endogenous stimulus
response to reactive oxygen species
response to lipid
positive regulation of gene expression
cellular response to oxidative stress
transmembrane receptor protein serine/threonine kinase signaling pathway
positive regulation of transcription from RNA polymerase II promoter
negative regulation of neuron apoptotic process
positive regulation of cellular biosynthetic process
transforming growth factor beta receptor signaling pathway

response to hormone
response to nitrogen compound
learning or memory
positive regulation of transcription, DNA-templated
positive regulation of nucleic acid-templated transcription
response to abiotic stimulus
positive regulation of RNA biosynthetic process
negative regulation of neuron death
transcription from RNA polymerase II promoter
positive regulation of cellular process
hormone-mediated signaling pathway
cellular response to reactive oxygen species
positive regulation of smooth muscle cell proliferation
response to transforming growth factor beta
cellular response to transforming growth factor beta stimulus
response to oxygen-containing compound
transcription initiation from RNA polymerase II promoter
cell death in response to hydrogen peroxide
negative regulation of response to reactive oxygen species
regulation of hydrogen peroxide-induced cell death
negative regulation of hydrogen peroxide-induced cell death
behavior
cognition
response to hydrogen peroxide
tissue development
maternal placenta development
type B pancreatic cell proliferation
regulation of smooth muscle cell proliferation
response to lipopolysaccharide
response to steroid hormone
response to molecule of bacterial origin
regulation of neuron apoptotic process
regulation of cellular amide metabolic process
smooth muscle cell proliferation
positive regulation of cell proliferation
cellular response to stress
regulation of cell proliferation
response to muscle stretch
negative regulation of muscle contraction
positive regulation of muscle contraction
negative regulation of smooth muscle contraction
negative regulation of cellular response to oxidative stress
negative regulation of response to oxidative stress

negative regulation of oxidative stress-induced cell death
response to cAMP
neuron apoptotic process
cellular response to chemical stimulus
regulation of biosynthetic process
cellular response to hormone stimulus
positive regulation of lipid metabolic process
regulation of neuron death
osteoblast proliferation
labyrinthine layer blood vessel development
regulation of response to reactive oxygen species
blood vessel morphogenesis
placenta development
regulation of cell death
negative regulation of cellular process
regulation of cell cycle
female pregnancy
cellular response to steroid hormone stimulus
regulation of cardiac muscle hypertrophy
positive regulation of fatty acid metabolic process
brown fat cell differentiation
regulation of oxidative stress-induced cell death
response to organic substance
positive regulation of epithelial cell proliferation
cell death
death
response to calcium ion
response to bacterium
neuron death
regulation of response to stimulus
response to chemical
cell migration involved in sprouting angiogenesis
regulation of muscle hypertrophy
positive regulation of biological process
negative regulation of transcription from RNA polymerase II promoter
regulation of macromolecule biosynthetic process
Fc-epsilon receptor signaling pathway
cellular developmental process
placenta blood vessel development
cellular response to hydrogen peroxide
regulation of response to stress
negative regulation of cell death
blood vessel development

cell death in response to oxidative stress
maternal process involved in female pregnancy
muscle cell proliferation
cellular response to metal ion
multi-multicellular organism process
response to metal ion
positive regulation of myeloid leukocyte differentiation
SMAD protein signal transduction
regulation of cellular response to oxidative stress
vasculature development
negative regulation of biological process
response to stress
cellular response to growth factor stimulus
regulation of smooth muscle contraction
myeloid leukocyte differentiation
response to growth factor
regulation of cellular biosynthetic process
cellular response to organic cyclic compound
skeletal muscle cell differentiation
regulation of response to oxidative stress
cellular response to inorganic substance
cell proliferation
positive regulation of multicellular organismal process
cellular response to organic substance
cardiac muscle hypertrophy
positive regulation of lipid biosynthetic process
response to radiation
Fc receptor signaling pathway
cell differentiation
cell surface receptor signaling pathway
muscle hypertrophy
striated muscle hypertrophy
regulation of muscle adaptation
cellular response to oxygen-containing compound
macromolecule biosynthetic process
positive regulation of myeloid cell differentiation
labyrinthine layer development
regulation of nitrogen compound metabolic process
intussusceptive angiogenesis
pyruvate oxidation
epithalamus development
positive regulation of cerebellar granule cell precursor proliferation
habenula development

positive regulation of translation in response to stress
positive regulation of translational initiation in response to stress
maintenance of blood-brain barrier
protein O-linked fucosylation
neuron death in response to hydrogen peroxide
eIF2alpha dephosphorylation in response to endoplasmic reticulum stress
positive regulation of mast cell activation by Fc-epsilon receptor signaling pathway
MHC class I biosynthetic process
regulation of MHC class I biosynthetic process
positive regulation of MHC class I biosynthetic process
NK T cell activation
regulation of NK T cell activation
positive regulation of NK T cell activation
general adaptation syndrome
vestibular reflex
regulation of endoplasmic reticulum stress-induced eIF2 alpha phosphorylation
platelet-derived growth factor production
regulation of platelet-derived growth factor production
positive regulation of platelet-derived growth factor production
regulation of hydrogen peroxide-induced neuron death
negative regulation of hydrogen peroxide-induced neuron death
negative regulation of PERK-mediated unfolded protein response
regulation of endoplasmic reticulum stress-induced eIF2 alpha dephosphorylation
positive regulation of endoplasmic reticulum stress-induced eIF2 alpha dephosphorylation
neurological system process
regulation of muscle system process
angiogenesis
cell-type specific apoptotic process
regulation of transcription from RNA polymerase II promoter in response to stress
regulation of neural precursor cell proliferation
positive regulation of response to stimulus
intracellular receptor signaling pathway
response to drug
cell cycle
anatomical structure formation involved in morphogenesis
regulation of translation
sprouting angiogenesis
regulation of cellular macromolecule biosynthetic process
muscle adaptation
regulation of DNA-templated transcription in response to stress
organ development
cellular amide metabolic process
positive regulation of endothelial cell proliferation

positive regulation of cellular amide metabolic process
blood vessel endothelial cell migration
response to temperature stimulus
cellular response to external stimulus
regulation of macromolecule metabolic process
response to external stimulus
toll-like receptor 5 signaling pathway
toll-like receptor 10 signaling pathway
cellular response to stimulus
negative regulation of apoptotic process
TRIF-dependent toll-like receptor signaling pathway
regulation of epithelial cell proliferation
negative regulation of programmed cell death
positive regulation of developmental process
MyD88-independent toll-like receptor signaling pathway
feeding behavior
toll-like receptor 9 signaling pathway
toll-like receptor TLR1:TLR2 signaling pathway
toll-like receptor TLR6:TLR2 signaling pathway
immune response-regulating cell surface receptor signaling pathway

Genes
NR4A1 NR4A2 NR4A3
NR4A1 NR4A2 NR4A3
NR4A1 NR4A2 NR4A3 PTGS2 RGS2
ARC BTG2 FOS JUN PTGS2
FOS GPR37L1 JUN NR4A2 NR4A3 PTGS2
JUN PPP1R15A
CYR61 FOS HSPH1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2
ARC BTG2 FOS JUN NR4A2 NR4A3 PTGS2
BTG2 FOS JUN JUNB PTGS2
BTG2 CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2
JUN JUNB NR4A1 NR4A2 NR4A3
BTG2 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PTGS2
BTG2 CYR61 FOS GPR37L1 HSPH1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2 RGS2 ZFAND2A
BTG2 CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A
NR4A1 NR4A2 NR4A3
FOS JUN JUNB PTGS2
CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2
CYR61 FOS HSPH1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A
BTG2 CYR61 FOS GPR37L1 HSPH1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A ZFAND2A
FOS GPR37L1 JUN JUNB NR4A3 PTGS2
FOS JUN JUNB
FOS JUN JUNB PTGS2
BTG2 CYR61 FOS GPR37L1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2 ZFAND2A
BTG2 CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A
JUNB PTGS2
NR4A1 NR4A3
JUN PPP1R15A
BTG2 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PTGS2
BTG2 CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A
BTG2 CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2
FOS GPR37L1 JUN NR4A3
FOS JUN JUNB NR4A1 NR4A2 NR4A3 PTGS2
BTG2 CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A
FOS GPR37L1 NR4A2 NR4A3
CYR61 FOS JUN JUNB PPP1R15A
CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3
BTG2 JUN NR4A2 NR4A3
CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2
FOS JUN JUNB PPP1R15A

BTG2 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PTGS2
BTG2 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PTGS2
ARC BTG2 FOS JUN PTGS2
CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A
CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A
BTG2 DNAJA4 FOS HSPH1 JUN JUNB NR4A2 PTGS2
CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A
BTG2 JUN NR4A2 NR4A3
BTG2 CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A
ARC BTG2 CYR61 FOS GPR37L1 HSPH1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2 RGS2 ZFAND2A
NR4A1 NR4A2 NR4A3
FOS GPR37L1 NR4A3
JUN NR4A3 PTGS2
FOS JUN JUNB PPP1R15A
FOS JUN JUNB PPP1R15A
BTG2 FOS GPR37L1 JUN JUNB NR4A1 NR4A2 NR4A3 PTGS2
JUNB NR4A1 NR4A2 NR4A3
GPR37L1 NR4A3
GPR37L1 NR4A3
GPR37L1 NR4A3
GPR37L1 NR4A3
ARC BTG2 FOS JUN NR4A2 NR4A3 PTGS2
ARC BTG2 FOS JUN PTGS2
GPR37L1 JUN NR4A3
APCDD1 ARC BTG2 CYR61 FOS JUN JUNB NR4A3 PTGS2
JUNB PTGS2
NR4A1 NR4A3
JUN NR4A3 PTGS2
FOS JUN JUNB PTGS2
FOS NR4A1 NR4A2 NR4A3 PTGS2
FOS JUN JUNB PTGS2
BTG2 JUN NR4A2 NR4A3
BTG2 CYR61 PPP1R15A RGS2
JUN NR4A3 PTGS2
CYR61 GPR37L1 JUN NR4A1 NR4A3 PTGS2
BTG2 FOS GPR37L1 HSPH1 JUN NR4A2 NR4A3 PPP1R15A PTGS2
BTG2 CYR61 GPR37L1 JUN JUNB NR4A1 NR4A3 PTGS2
FOS JUN
PTGS2 RGS2
PTGS2 RGS2
PTGS2 RGS2
GPR37L1 NR4A3
GPR37L1 NR4A3

GPR37L1 NR4A3
FOS JUN JUNB
BTG2 JUN NR4A2 NR4A3
CYR61 FOS GPR37L1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2 ZFAND2A
BTG2 CYR61 FOS HSPH1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2 RGS2
FOS JUN JUNB NR4A1 NR4A2 NR4A3
CYR61 NR4A3 PTGS2
BTG2 JUN NR4A2 NR4A3
CYR61 JUNB
CYR61 JUNB
GPR37L1 NR4A3
CYR61 JUN JUNB NR4A1 PTGS2
CYR61 JUNB PTGS2
BTG2 CYR61 GPR37L1 JUN JUNB NR4A2 NR4A3 PTGS2
APCDD1 BTG2 CYR61 DNAJA4 GPR37L1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2 RGS2
JUN JUNB NR4A1 NR4A3 PPP1R15A PTGS2
FOS JUNB PTGS2
NR4A1 NR4A2 NR4A3
NR4A3 RGS2
NR4A3 PTGS2
PTGS2 RGS2
GPR37L1 NR4A3
BTG2 CYR61 FOS HSPH1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2
JUN NR4A1 NR4A3
BTG2 CYR61 GPR37L1 JUN JUNB NR4A2 NR4A3 PPP1R15A PTGS2
BTG2 CYR61 GPR37L1 JUN JUNB NR4A2 NR4A3 PPP1R15A PTGS2
FOS JUN JUNB
FOS JUN JUNB PTGS2
BTG2 JUN NR4A2 NR4A3
APCDD1 ARC CYR61 FOS GPR37L1 HSPH1 JUN NR4A1 NR4A3 PPP1R15A PTGS2 RGS2
BTG2 CYR61 FOS GPR37L1 HSPH1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2 ZFAND2A
NR4A1 PTGS2
NR4A3 RGS2
ARC BTG2 CYR61 FOS GPR37L1 HSPH1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2 RGS2 ZFAND2A
BTG2 JUN JUNB NR4A3 PPP1R15A
BTG2 CYR61 FOS HSPH1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A RGS2
FOS JUN NR4A1 NR4A3
APCDD1 ARC BTG2 CYR61 FOS GPR37L1 JUN JUNB NR4A1 NR4A2 NR4A3 PTGS2 RGS2
CYR61 JUNB
GPR37L1 NR4A3
FOS GPR37L1 HSPH1 JUN NR4A3 PPP1R15A PTGS2
BTG2 CYR61 GPR37L1 JUN NR4A2 NR4A3
CYR61 JUN JUNB NR4A1 PTGS2

GPR37L1 NR4A3
JUNB PTGS2
JUN NR4A3 PTGS2
FOS JUN JUNB
FOS JUNB PTGS2
FOS JUN JUNB PTGS2
FOS JUN
FOS JUN
GPR37L1 NR4A3
CYR61 JUN JUNB NR4A1 PTGS2
APCDD1 BTG2 CYR61 DNAJA4 GPR37L1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2 RGS2
BTG2 CYR61 DNAJA4 FOS GPR37L1 HSPH1 JUN NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2
CYR61 FOS JUN JUNB NR4A1 PPP1R15A
PTGS2 RGS2
FOS JUN JUNB
CYR61 FOS JUN JUNB NR4A1 PPP1R15A
BTG2 CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2 RGS2
NR4A1 NR4A2 NR4A3 PTGS2
BTG2 FOS
GPR37L1 NR4A3
FOS JUN JUNB
BTG2 CYR61 GPR37L1 JUN JUNB NR4A1 NR4A3 PTGS2
CYR61 FOS GPR37L1 JUN NR4A3 PTGS2 RGS2
CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2
NR4A3 RGS2
CYR61 PTGS2
FOS JUN JUNB PTGS2
FOS JUN NR4A1 NR4A3
APCDD1 BTG2 CYR61 FOS GPR37L1 JUN JUNB NR4A1 NR4A2 NR4A3 PTGS2 RGS2
APCDD1 ARC CYR61 FOS GPR37L1 JUN JUNB NR4A1 NR4A3 PPP1R15A
NR4A3 RGS2
NR4A3 RGS2
NR4A3 RGS2
FOS GPR37L1 NR4A1 NR4A2 NR4A3 PTGS2
BTG2 CYR61 FOS HSPH1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A RGS2 SPON1
FOS JUN
CYR61 JUNB
BTG2 CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2 RGS2
CYR61
NR4A3
NR4A2
GPR37L1
NR4A2

PPP1R15A
PPP1R15A
PTGS2
SPON1
NR4A3
PPP1R15A
NR4A3
HSPH1
HSPH1
HSPH1
HSPH1
HSPH1
HSPH1
NR4A2
NR4A3
PPP1R15A
PTGS2
PTGS2
PTGS2
NR4A3
NR4A3
PPP1R15A
PPP1R15A
PPP1R15A
ARC BTG2 FOS JUN NR4A3 PTGS2
NR4A3 PTGS2 RGS2
CYR61 JUN NR4A1 PTGS2
BTG2 JUN NR4A2 NR4A3
JUN PPP1R15A
BTG2 GPR37L1
ARC CYR61 FOS GPR37L1 JUN NR4A3 PPP1R15A PTGS2
NR4A1 NR4A2 NR4A3
FOS JUN JUNB PTGS2
JUN JUNB NR4A1 NR4A3 PPP1R15A PTGS2 RGS2
CYR61 JUN JUNB NR4A1 NR4A3 PTGS2
BTG2 PPP1R15A RGS2
NR4A1 PTGS2
BTG2 CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A RGS2
NR4A3 RGS2
JUN PPP1R15A
APCDD1 BTG2 CYR61 FOS GPR37L1 JUN JUNB NR4A2 NR4A3 PTGS2
BTG2 CYR61 PPP1R15A PTGS2 RGS2
JUN NR4A1

CYR61 PPP1R15A
NR4A1 PTGS2
DNAJA4 FOS HSPH1
FOS JUN NR4A2 PTGS2
BTG2 CYR61 FOS GPR37L1 HSPH1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A RGS2 ZFAND2A
BTG2 CYR61 FOS JUN JUNB NR4A1 NR4A2 NR4A3 PTGS2
FOS JUN
FOS JUN
APCDD1 ARC BTG2 CYR61 FOS GPR37L1 HSPH1 JUN JUNB NR4A1 NR4A2 NR4A3 PPP1R15A PTGS2 RGS2 Z
BTG2 CYR61 JUN NR4A2 NR4A3
FOS JUN
JUN NR4A1 NR4A3
BTG2 CYR61 JUN NR4A2 NR4A3
CYR61 FOS GPR37L1 JUN JUNB PTGS2
FOS JUN
FOS NR4A3
FOS JUN
FOS JUN
FOS JUN
FOS JUN NR4A1 NR4A3

padjust
9.17E-05
9.17E-05
0.00497988
0.00497988
0.00497988
0.00497988
0.00497988
0.00497988
0.00497988
0.00497988
0.00497988
0.00534059
0.00534059
0.00534059
0.00534059
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.0072225
0.00747849

0.00762266
0.00819752
0.00819752
0.00848119
0.00848119
0.00848119
0.00848119
0.00848119
0.00848119
0.00848119
0.00848119
0.00848119
0.00848119
0.00892629
0.00892629
0.00918051
0.00953287
0.00953287
0.00953287
0.00953287
0.00953287
0.01053274
0.01068644
0.01078424
0.01114539
0.01209438
0.01209438
0.01348938
0.01396695
0.01396695
0.01419806
0.01419806
0.0146614
0.0146614
0.0146614
0.01488407
0.01488407
0.01629395
0.01629395
0.01629395
0.01629395
0.01629395
0.01629395

0.01629395
0.01629395
0.01629395
0.01766495
0.0178198
0.0178198
0.02058109
0.02058109
0.02210011
0.02210011
0.02210011
0.02210011
0.02210011
0.02210011
0.02249225
0.02249225
0.0227982
0.02374349
0.02374349
0.02374349
0.02374349
0.02374349
0.02416715
0.02416715
0.02450714
0.02450714
0.02498413
0.02518649
0.02518649
0.02529629
0.02529629
0.02529629
0.02529629
0.02576386
0.02652901
0.02652901
0.02696768
0.02729099
0.02773116
0.02773116
0.02832279
0.02832279
0.0306407

0.0306407
0.0306407
0.03127183
0.03127183
0.03267707
0.03276009
0.03308389
0.03308389
0.03308389
0.03346723
0.03454511
0.03523926
0.03603227
0.03603227
0.03853845
0.03853845
0.03873634
0.03873634
0.03873634
0.03873634
0.03890015
0.03957797
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161

0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04035161
0.04114923
0.04124228
0.04229175
0.04229175
0.04229175
0.04229175
0.0430584
0.04329247
0.04370211
0.04371555
0.04406126
0.04411332
0.0445969
0.04695061
0.0477984
0.0477984
0.04791273
0.04979794
0.05057502

0.05057502
0.05057502
0.05057502
0.05177467
0.05284515
0.05476899
0.05719013
0.05719013
0.05724592
0.05724592
0.05724592
0.05724592
0.05724592
0.05724592
0.05724592
0.05724592
0.05724592
0.05724592
0.05724592
0.05724592

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0006457	8.54E-14	37.7299771	0.5730897	12	69
GO:0006986	2.15E-13	43.0729167	0.45681063	11	55
GO:0035966	3.28E-13	41.1802536	0.47342193	11	57
GO:0009408	4.78E-09	28.4995693	0.42358804	8	51
GO:0009266	7.64E-09	20.6187291	0.64784053	9	78
GO:0042026	2.23E-08	99.3333333	0.09966777	5	12
GO:0061077	1.69E-07	57.875	0.14119601	5	17
GO:0044267	5.44E-06	4.89174131	10.9053156	24	1313
GO:0019538	8.64E-06	4.80594406	12.0847176	25	1455
GO:0034605	9.21E-06	22.3010753	0.29900332	5	36
GO:0009628	1.67E-05	5.761684	2.98172757	12	359
GO:0018126	2.86E-05	78.2625	0.06644518	3	8
GO:1900034	4.46E-05	25.5483871	0.2076412	4	25
GO:0017185	6.70E-05	Inf	0.0166113	2	2
GO:0070389	6.70E-05	Inf	0.0166113	2	2
GO:0051085	0.00020004	253.212121	0.02491694	2	3
GO:0044260	0.00021152	3.91395349	16.2956811	27	1962
GO:0006950	0.00023624	3.52976473	8.89534884	19	1071
GO:0044237	0.00034146	4.96085165	21.4202658	31	2579
GO:1900101	0.00039798	126.575758	0.03322259	2	4
GO:0071704	0.00047116	4.79833398	21.6943522	31	2612
GO:0080135	0.0005809	5.75431034	1.50332226	7	181
GO:0036500	0.00065984	84.3636364	0.04152824	2	5
GO:1990440	0.00065984	84.3636364	0.04152824	2	5
GO:0030433	0.00072565	20.5263158	0.18272425	3	22
GO:0036503	0.00082976	19.4953125	0.1910299	3	23
GO:0044238	0.00083001	4.07797428	20.9136213	30	2518
GO:0051604	0.00086015	7.83908046	0.7641196	5	92
GO:0043065	0.00088067	5.3368984	1.61129568	7	194
GO:0043068	0.00093607	5.27777778	1.62790698	7	196
GO:0043170	0.00101673	3.36371237	17.6079734	27	2120
GO:0010942	0.00132936	4.94776119	1.72757475	7	208
GO:0071236	0.00137126	50.5939394	0.05813953	2	7
GO:0071353	0.00181882	42.1515152	0.06644518	2	8
GO:0010033	0.00190155	2.99015513	7.08471761	15	853
GO:0070670	0.0023263	36.1212121	0.07475083	2	9
GO:0050790	0.00268968	3.00881262	5.80564784	13	699
GO:0036003	0.00289274	31.5984848	0.08305648	2	10
GO:0042149	0.00289274	31.5984848	0.08305648	2	10
GO:0097237	0.00289274	31.5984848	0.08305648	2	10

GO:0010824	0.00351718	28.0808081	0.09136213	2	11
GO:0046605	0.00351718	28.0808081	0.09136213	2	11
GO:0008152	0.00369138	4.34208754	24.9335548	32	3002
GO:0051084	0.00419866	25.2666667	0.09966777	2	12
GO:0050714	0.00420275	10.4949324	0.33222591	3	40
GO:0006458	0.00493626	22.9641873	0.10797342	2	13
GO:0032755	0.00493626	22.9641873	0.10797342	2	13
GO:0042116	0.00572905	21.0454545	0.11627907	2	14
GO:1901998	0.00572905	21.0454545	0.11627907	2	14
GO:0030199	0.00657612	19.4219114	0.12458472	2	15
GO:0046677	0.00657612	19.4219114	0.12458472	2	15
GO:0002377	0.00747656	18.030303	0.13289037	2	16
GO:0000056	0.00830565	Inf	0.00830565	1	1
GO:0001980	0.00830565	Inf	0.00830565	1	1
GO:0002014	0.00830565	Inf	0.00830565	1	1
GO:0002236	0.00830565	Inf	0.00830565	1	1
GO:0002368	0.00830565	Inf	0.00830565	1	1
GO:0002418	0.00830565	Inf	0.00830565	1	1
GO:0002424	0.00830565	Inf	0.00830565	1	1
GO:0002834	0.00830565	Inf	0.00830565	1	1
GO:0002836	0.00830565	Inf	0.00830565	1	1
GO:0002837	0.00830565	Inf	0.00830565	1	1
GO:0002839	0.00830565	Inf	0.00830565	1	1
GO:0002840	0.00830565	Inf	0.00830565	1	1
GO:0002842	0.00830565	Inf	0.00830565	1	1
GO:0006398	0.00830565	Inf	0.00830565	1	1
GO:0006987	0.00830565	Inf	0.00830565	1	1
GO:0007518	0.00830565	Inf	0.00830565	1	1
GO:0015993	0.00830565	Inf	0.00830565	1	1
GO:0018395	0.00830565	Inf	0.00830565	1	1
GO:0019889	0.00830565	Inf	0.00830565	1	1
GO:0033133	0.00830565	Inf	0.00830565	1	1
GO:0046946	0.00830565	Inf	0.00830565	1	1
GO:0046947	0.00830565	Inf	0.00830565	1	1
GO:0060096	0.00830565	Inf	0.00830565	1	1
GO:0060690	0.00830565	Inf	0.00830565	1	1
GO:0060691	0.00830565	Inf	0.00830565	1	1
GO:0060904	0.00830565	Inf	0.00830565	1	1
GO:0070077	0.00830565	Inf	0.00830565	1	1
GO:0070078	0.00830565	Inf	0.00830565	1	1
GO:0070079	0.00830565	Inf	0.00830565	1	1
GO:0071492	0.00830565	Inf	0.00830565	1	1
GO:0090074	0.00830565	Inf	0.00830565	1	1

GO:0100032	0.00830565	Inf	0.00830565	1	1
GO:1900098	0.00830565	Inf	0.00830565	1	1
GO:1900100	0.00830565	Inf	0.00830565	1	1
GO:1900413	0.00830565	Inf	0.00830565	1	1
GO:1903301	0.00830565	Inf	0.00830565	1	1
GO:1903332	0.00830565	Inf	0.00830565	1	1
GO:1903487	0.00830565	Inf	0.00830565	1	1
GO:1903489	0.00830565	Inf	0.00830565	1	1
GO:1903891	0.00830565	Inf	0.00830565	1	1
GO:1903894	0.00830565	Inf	0.00830565	1	1
GO:1990418	0.00830565	Inf	0.00830565	1	1
GO:2000298	0.00830565	Inf	0.00830565	1	1
GO:2000299	0.00830565	Inf	0.00830565	1	1
GO:2000347	0.00830565	Inf	0.00830565	1	1
GO:0002312	0.00842948	16.8242424	0.14119601	2	17
GO:0006888	0.00842948	16.8242424	0.14119601	2	17
GO:0006984	0.00842948	16.8242424	0.14119601	2	17
GO:0036498	0.00842948	16.8242424	0.14119601	2	17
GO:0050896	0.00876379	2.55169996	18.6461794	26	2245
GO:0032675	0.00943399	15.7689394	0.14950166	2	18

Term	Genes	padjust
protein foldin	BAG2 CHORD	1.24E-10
response to u	DNAJA1 DNA	1.57E-10
response to t	DNAJA1 DNA	1.59E-10
response to h	BAG2 CHORD	1.74E-06
response to t	BAG2 CHORD	2.22E-06
protein refolc	DNAJA1 DNA	5.41E-06
chaperone-m	CHORDC1 DN	3.52E-05
cellular prote	APH1B BAG2	0.00098958
protein metal	APH1B BAG2	0.00133994
cellular respo	BAG2 CHORD	0.00133994
response to a	BAG2 CHORD	0.00221106
protein hydrc	JMJD6 P4HA1	0.00346537
regulation of	BAG2 CHORD	0.00499121
peptidyl-lysin	JMJD6 PLOD1	0.00650179
chaperone co	DNAJB1 PTGE	0.00650179
chaperone m	DNAJB1 HSPD	0.01810385
cellular macr	APH1B BAG2	0.01810385
response to s	AHSA1 BAG2	0.01909602
cellular metal	ADHFE1 APH	0.02614859
regulation of	HSPA5 XBP1	0.02895327
organic subst	ADHFE1 APH	0.03264438
regulation of	BAG2 CHORD	0.0384187
ATF6-mediat	HSPA5 XBP1	0.04000304
positive regul	HSPA5 XBP1	0.04000304
ER-associatec	HSPA5 TME	0.04223288
ERAD pathwa	HSPA5 TME	0.04418533
primary meta	APH1B BAG2	0.04418533
protein matu	APH1B HSPD	0.04418533
positive regul	APH1B DEDD	0.04418533
positive regul	APH1B DEDD	0.04539959
macromolecu	APH1B BAG2	0.04772051
positive regul	APH1B DEDD	0.06044421
cellular respo	HSPA5 XBP1	0.06046006
cellular respo	HSPA5 XBP1	0.07783474
response to c	APH1B DNAJ	0.07905028
response to i	HSPA5 XBP1	0.09402138
regulation of	AHSA1 APH1	0.10522344
positive regul	HSPA5 XBP1	0.10522344
cellular respo	HSPA5 XBP1	0.10522344
cellular respo	HSPA5 XBP1	0.10522344

regulation of	CHORDC1 XP	0.12143454
regulation of	CHORDC1 XP	0.12143454
metabolic pr	ADHFE1 AHS	0.12143454
'de novo' pos	DNAJB1 HSPD	0.12143454
positive regul	PFKFB2 PPID	0.12143454
'de novo' pro	DNAJB1 HSPD	0.12143454
positive regul	HSPD1 XBP1	0.12143454
macrophage	HSPD1 JMJD6	0.12143454
toxin transpo	DNAJA1 HSPA	0.12143454
collagen fibril	P4HA1 SERPI	0.12143454
response to a	HSPA5 XBP1	0.12143454
immunoglobu	HSPD1 XBP1	0.12143454
ribosomal sm	XPO1	0.12143454
regulation of	MANF	0.12143454
vasoconstrict	MANF	0.12143454
detection of	HSPD1	0.12143454
B cell cytokin	HSPD1	0.12143454
immune resp	HSPD1	0.12143454
T cell mediat	HSPD1	0.12143454
regulation of	HSPD1	0.12143454
positive regul	HSPD1	0.12143454
regulation of	HSPD1	0.12143454
positive regul	HSPD1	0.12143454
regulation of	HSPD1	0.12143454
positive regul	HSPD1	0.12143454
histone mRN	ZNF473	0.12143454
activation of	HSPA5	0.12143454
myoblast fate	IFRD1	0.12143454
molecular hy	ADHFE1	0.12143454
peptidyl-lysin	JMJD6	0.12143454
pteridine me	SPR	0.12143454
positive regul	PFKFB2	0.12143454
hydroxylysine	PLOD1	0.12143454
hydroxylysine	PLOD1	0.12143454
serotonin sec	XBP1	0.12143454
epithelial cell	XBP1	0.12143454
epithelial cell	XBP1	0.12143454
regulation of	HSPA5	0.12143454
histone argini	JMJD6	0.12143454
histone H3-R	JMJD6	0.12143454
histone H4-R	JMJD6	0.12143454
cellular respo	PPID	0.12143454
negative regu	HSPA5	0.12143454

positive regul	XBP1	0.12143454
regulation of	XBP1	0.12143454
positive regul	XBP1	0.12143454
positive regul	XBP1	0.12143454
positive regul	PFKFB2	0.12143454
regulation of	HSPA5	0.12143454
regulation of	XBP1	0.12143454
positive regul	XBP1	0.12143454
regulation of	HSPA5	0.12143454
regulation of	HSPA5	0.12143454
response to i	XBP1	0.12143454
regulation of	CHORDC1	0.12143454
negative regu	CHORDC1	0.12143454
positive regul	XBP1	0.12143454
B cell activati	HSPD1 XBP1	0.12143454
ER to Golgi ve	LMAN2L LMF	0.12143454
ER-nucleus si	HSPA5 XBP1	0.12143454
IRE1-mediate	HSPA5 XBP1	0.12143454
response to s	AHSA1 APH1E	0.12501292
regulation of	HSPD1 XBP1	0.13326657

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0007402	0.00213574	Inf	0.00213574	1	1
GO:0006030	0.00426742	525.5	0.00427148	1	2
GO:0006032	0.00426742	525.5	0.00427148	1	2
GO:0048865	0.00426742	525.5	0.00427148	1	2
GO:0048867	0.00426742	525.5	0.00427148	1	2
GO:0009313	0.00639505	262.6875	0.00640721	1	3
GO:0032460	0.00639505	262.6875	0.00640721	1	3
GO:0034214	0.00639505	262.6875	0.00640721	1	3
GO:1901072	0.00639505	262.6875	0.00640721	1	3
GO:0009636	0.00740197	19.4098361	0.1345515	2	63
GO:0038003	0.00851865	175.083333	0.00854295	1	4
GO:0045899	0.00851865	175.083333	0.00854295	1	4
GO:0046348	0.00851865	175.083333	0.00854295	1	4
GO:0060261	0.00851865	175.083333	0.00854295	1	4

Term	**Genes**
ganglion mother cell fate determination	POU6F2
chitin metabolic process	CTBS
chitin catabolic process	CTBS
stem cell fate commitment	POU6F2
stem cell fate determination	POU6F2
oligosaccharide catabolic process	CTBS
negative regulation of protein oligomerization	OPRD1
protein hexamerization	PANX2
glucosamine-containing compound catabolic process	CTBS
response to toxic substance	AHR OPRD1
opioid receptor signaling pathway	OPRD1
positive regulation of RNA polymerase II transcriptional preinitiation complex assembly	AHR
amino sugar catabolic process	CTBS
positive regulation of transcription initiation from RNA polymerase II promoter	AHR

padjust
0.21844242
0.21844242
0.21844242
0.21844242
0.21844242
0.21844242
0.21844242
0.21844242
0.21844242
0.21844242
0.21844242
0.21844242
0.21844242
0.21844242

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size
GO:0001580	0.00189776	1403	0.00189843	1	4
GO:0050912	0.00189776	1403	0.00189843	1	4
GO:0050913	0.00237192	1052	0.00237304	1	5
GO:0050909	0.00426742	525.5	0.00427148	1	9
GO:0050907	0.00663427	323	0.00664452	1	14
GO:0007585	0.00994312	209.6	0.00996678	1	21

Term	Genes	padjust
detection of c	TAS2R4	0.04032257
detection of c	TAS2R4	0.04032257
sensory perce	TAS2R4	0.04032257
sensory perce	TAS2R4	0.05440961
detection of c	TAS2R4	0.06766952
respiratory ga	TAS2R4	0.07773481